

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:21:40 / Search time 13.0223 Seconds

(without alignments)
155.160 Million cell updates/sec

Title: US-09-642-744d-19

Sequence: 1 GLRRLKFRNKIKELKKIG 21

Scoring table:

BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

PIR 791*
1: p1r1*
2: p1r2*
3: p1r3*
4: p1r4*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|----------------------|
| 1 | 104 | 100.0 | 171 | 2 JQ1171 | 18K lipopolysaccha |
| 2 | 54 | 51.9 | 42 | 2 S65524 | antibacterial prot |
| 3 | 53 | 51.0 | 3411 | 1 GNMVY | genome polypeptide |
| 4 | 53 | 51.0 | 3411 | 1 GNMVY | genome polypeptide |
| 5 | 52 | 50.0 | 1163 | 1 GNMVY | genome polypeptide |
| 6 | 51.5 | 49.5 | 976 | 2 A97104 | zinc-dependent metal |
| 7 | 51 | 49.0 | 241 | 2 G86355 | hypothetical prote |
| 8 | 50 | 48.1 | 162 | 2 H70314 | hypothetical prote |
| 9 | 50 | 48.1 | 162 | 2 H70314 | hypothetical prote |
| 10 | 50 | 48.1 | 173 | 2 S70521 | antibacterial prot |
| 11 | 50 | 48.1 | 213 | 2 B83979 | hypothetical prote |
| 12 | 50 | 48.1 | 213 | 2 B83979 | hypothetical prote |
| 13 | 49.5 | 47.6 | 831 | 2 S44843 | hypothetical prote |
| 14 | 49.5 | 47.6 | 831 | 2 S44843 | hypothetical prote |
| 15 | 49.5 | 47.6 | 932 | 2 A75052 | leucyl-tRNA synthet |
| 16 | 49 | 47.1 | 142 | 2 F69552 | myoglobin - Balkal |
| 17 | 49 | 47.1 | 153 | 2 F69552 | myoglobin - Balkal |
| 18 | 49 | 47.1 | 324 | 2 T07982 | probable choline-p |
| 19 | 49 | 47.1 | 324 | 2 T07982 | probable choline-p |
| 20 | 49 | 47.1 | 655 | 2 S57119 | hypothetical prote |
| 21 | 48 | 46.2 | 288 | 2 JN0466 | epimerophan - human |
| 22 | 47.5 | 45.7 | 297 | 2 B90061 | hypothetical prote |
| 23 | 47.5 | 45.7 | 297 | 2 B90061 | hypothetical prote |
| 24 | 47.5 | 45.7 | 274 | 2 B90546 | conserved hypochet |
| 25 | 47.5 | 45.7 | 274 | 2 B90546 | conserved hypochet |
| 26 | 47 | 45.2 | 73 | 2 D64373 | hypothetical prote |
| 27 | 47 | 45.2 | 121 | 2 T03182 | hypothetical prote |
| 28 | 47 | 45.2 | 174 | 2 H70471 | conserved hypochet |
| 29 | 47 | 45.2 | 259 | 2 S57283 | 14-3-3 brain prote |
| | | | 705 | 2 F70475 | Vaob protein (tribo |

ALIGNMENTS

| | | | | | |
|----|----|------|------|----------|--------------------|
| 30 | 47 | 45.2 | 766 | 2 A75332 | probable DNA mima |
| 31 | 47 | 45.2 | 1137 | 2 G84581 | copla-like retroel |
| 32 | 47 | 45.2 | 1233 | 2 I54383 | chromosome segrega |
| 33 | 46 | 44.2 | 153 | 1 MYBD | myoglobin - Bursai |
| 34 | 46 | 44.2 | 153 | 1 MYDG | myoglobin - dog (c |
| 35 | 46 | 44.2 | 153 | 1 MYDGAH | myoglobin - Africa |
| 36 | 46 | 44.2 | 153 | 1 MYELA | myoglobin - Indian |
| 37 | 46 | 44.2 | 153 | 1 MYELI | myoglobin - bat-ea |
| 38 | 46 | 44.2 | 153 | 1 MYFBE | myoglobin - Cape f |
| 39 | 46 | 44.2 | 153 | 1 MYFBC | myoglobin - weasel |
| 40 | 46 | 44.2 | 153 | 1 MYLEM | myoglobin - gray s |
| 41 | 46 | 44.2 | 153 | 1 MYSLG | myoglobin (validat |
| 42 | 46 | 44.2 | 153 | 1 MYSLH | polypeptide deform |
| 43 | 46 | 44.2 | 169 | 2 A82373 | hypothetical prote |
| 44 | 46 | 44.2 | 305 | 2 T23829 | probable choline-p |
| 45 | 46 | 44.2 | 329 | 2 T07981 | |

RESULT 1

JQ1171

18K lipopolysaccharide-binding protein precursor - rabbit

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 06-Dec-1996

R/Accession: JQ1171, P80226

R/Author: J.W. Morgan, J.G. Palings, I. Hira, M. Yen, M.H.

A/Title: Complementary DNA sequence of rabbit CAP18-a unique lipopolysaccharide binding

A/Reference number: JQ1171, PMID:91354246, PMID:1883348

A/Accession: JQ1171

A/Molecule type: mRNA

A/Residues: 1-171 <LAR>

A/Experimental source: bone marrow

A/Accession: P80226

A/Molecule type: protein

A/Residues: 135-159, 'QIGQL' <LA2>

A/Note: 157-Asp was also found

C/Superfamily: cathelin; cystatin homology

F1-29/Domain: signal sequence #status predicted <SIG>

F/30-171/Product: 18K lipopolysaccharide-binding protein #status predicted <MAR>

Query Match

Best Local Similarity 100.0%; Score 104; DB 2; Length 171;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRRLKFRNKIKELKKIG 21

DB 135 GLRRLKFRNKIKELKKIG 155

RESULT 2

S65524

antibacterial protein, 11X - guinea pig (fragment)

C/Species: Cavia porcellus (guinea pig)

C/Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004

R/Accession: S65524

R/Author: S. Nagaoka, I. Yamashita, T.

A/Title: Purification of the 11- and 5-kDa antibacterial polypeptides from guinea pig n

A/Reference number: S65524, PMID:8644997

A/Accession: S65524

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-42 <YOM>

A/Cross-references: UNIPROT:Q91X12

Query Match

Best Local Similarity 51.9%; Score 54; DB 2; Length 42;

Matches 11; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:17:06 / Search time 65.5223 Seconds
(without alignments)
164.122 Million cell updates/sec

Title: US-09-642-744D-19

Perfect score: 104

Sequence: 1 GAKRRLKRFNKKIKKKIG 21

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: UniProt_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 104 | 100.0 | 171 | 1 | CP18_RABIT |
| 2 | 55 | 52.9 | 153 | 2 | P25230 oryctolagus |
| 3 | 54 | 51.9 | 178 | 2 | O82267 pyrobaculum |
| 4 | 53 | 51.0 | 400 | 2 | O91X12 cavia porce |
| 5 | 53 | 51.0 | 400 | 2 | O89295 yellow feve |
| 6 | 53 | 51.0 | 400 | 2 | O89297 yellow feve |
| 7 | 53 | 51.0 | 400 | 2 | O89299 yellow feve |
| 8 | 53 | 51.0 | 400 | 2 | O89304 yellow feve |
| 9 | 53 | 51.0 | 400 | 2 | O89311 yellow feve |
| 10 | 53 | 51.0 | 400 | 2 | O89317 yellow feve |
| 11 | 53 | 51.0 | 631 | 2 | O7RDG3 plasmodium |
| 12 | 53 | 51.0 | 778 | 2 | P89915 yellow feve |
| 13 | 53 | 51.0 | 778 | 2 | O77X62 yellow feve |
| 14 | 53 | 51.0 | 778 | 2 | O77X64 yellow feve |
| 15 | 53 | 51.0 | 809 | 2 | O9W9B8 yellow feve |
| 16 | 53 | 51.0 | 809 | 2 | O6FTT3 yellow feve |
| 17 | 53 | 51.0 | 3411 | 1 | POLG_YEPV1 |
| 18 | 53 | 51.0 | 3411 | 1 | POLG_YEPV2 |
| 19 | 53 | 51.0 | 3411 | 2 | O91857 yellow feve |
| 20 | 53 | 51.0 | 3411 | 2 | O98803 yellow feve |
| 21 | 53 | 51.0 | 3411 | 2 | O6DVH8 yellow feve |
| 22 | 53 | 51.0 | 3411 | 2 | O6J3P1 yellow feve |
| 23 | 53 | 51.0 | 3411 | 2 | O6PX46 yellow feve |
| 24 | 53 | 51.0 | 3411 | 2 | O89275 yellow feve |
| 25 | 53 | 51.0 | 3411 | 2 | O89276 yellow feve |
| 26 | 53 | 51.0 | 3411 | 2 | O89277 yellow feve |
| 27 | 53 | 51.0 | 3411 | 2 | O89278 yellow feve |
| 28 | 53 | 51.0 | 3411 | 2 | O9YRV3 yellow feve |
| 29 | 53 | 51.0 | 3411 | 2 | O9YRV3 yellow feve |
| 30 | 53 | 51.0 | 3411 | 2 | O9YVW1 yellow feve |
| 31 | 53 | 51.0 | 3411 | 2 | O9YVW2 yellow feve |
| 32 | 52 | 50.0 | 249 | 2 | O8C8U4 mus musculi |

| | | | | | | |
|----|------|------|------|---|------------|---------------------|
| 32 | 52 | 50.0 | 307 | 2 | Q7RLD2 | Q7RLD2 plasmodium |
| 33 | 52 | 50.0 | 364 | 2 | Q7RMJ3 | Q7RMJ3 plasmodium |
| 34 | 52 | 50.0 | 400 | 2 | O89315 | O89315 yellow feve |
| 35 | 52 | 50.0 | 1163 | 1 | POLG_YEPV8 | P29165 yellow feve |
| 36 | 51.5 | 49.5 | 976 | 2 | O971I7 | O971I7 clostridium |
| 37 | 51 | 49.0 | 205 | 2 | O6FIM8 | O6FIM8 candida gla |
| 38 | 51 | 49.0 | 228 | 2 | Q7AMC7 | Q7AMC7 nanocarchaeu |
| 39 | 51 | 49.0 | 241 | 2 | Q7G888 | Q7G888 arabidopsis |
| 40 | 51 | 49.0 | 301 | 2 | Q7RBE0 | Q7RBE0 plasmodium |
| 41 | 51 | 49.0 | 314 | 2 | Q7RI81 | Q7RI81 plasmodium |
| 42 | 51 | 49.0 | 400 | 2 | O89308 | O89308 yellow feve |
| 43 | 51 | 49.0 | 400 | 2 | O89309 | O89309 yellow feve |
| 44 | 51 | 49.0 | 575 | 2 | O8EW11 | O8EW11 mycoplasma |
| 45 | 50 | 48.1 | 113 | 2 | Q7RA52 | Q7RA52 plasmodium |

ALIGNMENTS

RESULT 1
ID CP18_RABIT STANDARD; PRT; 171 AA.
AC P25230;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Antimicrobial protein CAP18 precursor (18 kDa lipopolysaccharide-binding protein) (18 kDa cationic protein) (CAP18-A).
GN Name=CAP18;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_Taxid=9986;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 135-159.
RC TISSUE=Bone marrow;
RX MEDLINE=91354246; PubMed=1883348;
RA Larrick J.W., Morgan J.G., Palings I., Hirata M., Yen M.H.;
RT "Complementary DNA sequence of rabbit CAP18 -- a unique lipopolysaccharide binding protein.";
RL Biochem. Biophys. Res. Commun. 179:170-175(1991).
RN [2]
RP SEQUENCE OF 135-159, AND CHARACTERIZATION.
RX MEDLINE=94178952; PubMed=8132348;
RA Hirata M., Shimomura Y., Yoshida M., Morgan J.G., Palings I., Wilson D., Yen M.H., Wright S.C., Larrick J.W.;
RT "Characterization of a rabbit cationic protein (CAP18) with lipopolysaccharide-inhibitory activity.";
RL Infect. Immun. 62:1421-1426(1994).
RN [3]
RP SEQUENCE OF 135-154, AND CHARACTERIZATION.
RX MEDLINE=94075827; PubMed=8254193;
RA Larrick J.W., Hirata M., Zheng H., Zhong J., Bolin D., Cavallion J.-M., Warren H.S., Wright S.C.;
RT "A novel granulocyte-derived peptide with lipopolysaccharide-neutralizing activity.";
RL J. Immunol. 152:231-240(1994).
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=94148064; PubMed=8313956; DOI=10.1016/0014-5793(94)80395-1;
RA Tosi A., Scocchi M., Skerlavaj B., Gennaro R.;
RT "Identification and characterization of a primary antibacterial domain in CAP18, a lipopolysaccharide binding protein from rabbit leukocytes.";
RL FEBS Lett. 339:108-112(1994).
RN [5]
RP STRUCTURE BY NMR OF 135-166.
RX MEDLINE=55377455; PubMed=7649303; DOI=10.1016/0014-5793(95)00792-8;
RA Chen C., Brock R., Luh F., Chou P.-J., Larrick J.W., Huang R.-F., Huang T.-H.;
RT "The solution structure of the active domain of CAP18 -- a lipopolysaccharide binding protein from rabbit leukocytes.";
RL FEBS Lett. 370:46-52(1995).

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:21:40 ; Search time 17.9832 Seconds

(without alignments)
155.160 Million cell updates/sec

Title: US-09-642-744D-28

Sequence: 1 KMLRRIKRIHIKKYGPITIRIRIG 29

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|-------|-------------|--------|----|--------|---------------------|
| 1 | 103 | 72.5 | 152 | 2 | S68411 | cathelin-related p |
| 2 | 103 | 72.5 | 160 | 2 | S68412 | cathelin-related p |
| 3 | 103 | 72.5 | 160 | 2 | S68228 | myeloid antimicrob |
| 4 | 56.5 | 39.8 | 152 | 2 | A72385 | arginine repressor |
| 5 | 50 | 35.2 | 286 | 2 | D70403 | ferredoxin oxidore |
| 6 | 50 | 35.2 | 297 | 2 | H70446 | UTP-glucose-1-phos |
| 7 | 49.5 | 34.9 | 617 | 2 | T15104 | hypothetical protei |
| 8 | 49 | 34.5 | 266 | 2 | P75119 | hypothetical protei |
| 9 | 49 | 34.5 | 363 | 2 | T44564 | probable thiamin b |
| 10 | 49 | 34.5 | 429 | 2 | D90428 | hypothetical protei |
| 11 | 49 | 34.5 | 988 | 2 | A40628 | probable transpos |
| 12 | 49 | 34.5 | 1896 | 1 | RNF2L | DNA-directed RNA p |
| 13 | 48 | 33.8 | 181 | 2 | T15378 | hypothetical protei |
| 14 | 48 | 33.8 | 346 | 2 | F69109 | conserved hypothet |
| 15 | 48 | 33.8 | 406 | 2 | A71965 | hypothetical protei |
| 16 | 48 | 33.8 | 483 | 2 | AE1189 | beta-glucosidase h |
| 17 | 48 | 33.8 | 483 | 2 | AP1547 | beta-glucosidase h |
| 18 | 48 | 33.8 | 529 | 2 | T48253 | myb-like protein - |
| 19 | 48 | 33.8 | 572 | 2 | AC1200 | phosphotransferase |
| 20 | 48 | 33.8 | 590 | 2 | B89982 | phosphotransferase |
| 21 | 47.5 | 33.5 | 290 | 2 | D84651 | hypothetical protei |
| 22 | 47.5 | 33.5 | 456 | 2 | S58584 | hypothetical protei |
| 23 | 47 | 33.1 | 171 | 2 | H72405 | ribosomal protein |
| 24 | 47 | 33.1 | 181 | 2 | B90246 | hypoxanthine phosph |
| 25 | 47 | 33.1 | 213 | 2 | A30302 | sodium channel prot |
| 26 | 47 | 33.1 | 247 | 2 | T30008 | hypothetical protei |
| 27 | 47 | 33.1 | 295 | 2 | A56595 | sodium channel alpi |
| 28 | 47 | 33.1 | 295 | 2 | A56595 | sodium channel alpi |
| 29 | 47 | 33.1 | 428 | 2 | S35215 | sodium channel prot |

| | | | | | |
|----|------|------|------|----------|--------------------|
| 30 | 47 | 33.1 | 440 | 1 T06837 | protechlorophyllid |
| 31 | 47 | 33.1 | 686 | 2 T14203 | NADH2 dehydrogenas |
| 32 | 47 | 33.1 | 1689 | 2 S72467 | sodium channel pro |
| 33 | 47 | 33.1 | 1784 | 2 T43167 | sodium channel pro |
| 34 | 47 | 33.1 | 1820 | 2 A33299 | sodium channel pro |
| 35 | 47 | 33.1 | 2108 | 2 S72458 | sodium channel pro |
| 36 | 46.5 | 32.7 | 1570 | 2 T06754 | DNA-directed RNA p |
| 37 | 46 | 32.4 | 143 | 1 R3R211 | ribosomal protein |
| 38 | 46 | 32.4 | 240 | 2 A95327 | probable response |
| 39 | 46 | 32.4 | 293 | 2 B71012 | hypothetical prote |
| 40 | 46 | 32.4 | 319 | 1 S19248 | RNA-directed DNA p |
| 41 | 46 | 32.4 | 319 | 2 C97806 | hypothetical prote |
| 42 | 46 | 32.4 | 422 | 2 A99285 | hypothetical prote |
| 43 | 46 | 32.4 | 442 | 2 S73472 | probable thiophene |
| 44 | 46 | 32.4 | 490 | 2 S44545 | SSH1 protein - yea |
| 45 | 46 | 32.4 | 570 | 1 C46238 | phosphotransferase |

ALIGNMENTS

RESULT 1

S68411

Cathelin-related protein 2 precursor - sheep (fragment)

C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C/Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000

C/Accession: S68411

R/Mahoney, M.M.; Lee, A.Y.; Brezinski-Caliguri, D.J.; Huttner, K.M.

A/Title: Molecular analysis of the sheep cathelin family reveals a novel antimicrobial

A/Reference number: S68411; MUID:96140581; PMID:8549789

A/Accession: S68411

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-152 <MAH>

A/Cross-references: EMBL:X92757

C/Genetics:

A/Gene: SC5-2

C/Superfamily: cathelin; cystatin homology

F/1-21/Domain: signal sequence #status predicted <SIG>

F/14-123/Domain: cystatin homology <CYS>

F/21-123/Domain: propeptide #status predicted <PRO>

F/124-152/Product: cathelin-related protein 2 #status predicted <MAT>

Query Match Best local similarity 72.5%; Score 103; DB 2; Length 152; Pred. No. 9.1e-07; Matches 20; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 KMLRRIKRIHIKKYGPITIRIRIG 29

DB 124 RGLRLGRKRIAGVKYGPVIRIRIRIG 152

RESULT 2

S68412

Cathelin-related protein 1 precursor - sheep

C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C/Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000

C/Accession: S68412

R/Mahoney, M.M.; Lee, A.Y.; Brezinski-Caliguri, D.J.; Huttner, K.M.

A/Title: Molecular analysis of the sheep cathelin family reveals a novel antimicrobial

A/Reference number: S68411; MUID:96140581; PMID:8549789

A/Accession: S68412

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-160 <MAH>

A/Cross-references: EMBL:X92758

C/Genetics:

A/Gene: SC5-1

C/Superfamily: cathelin; cystatin homology

F/1-29/Domain: signal sequence #status predicted <SIG>

F/22-130/Domain: cystatin homology <CYS>

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OM protein - protein search, using SW model

Run on: May 2, 2005, 12:17:06 ; Search time 90.4832 Seconds
(without alignments)
164.122 Million cell updates/sec

Title: US-09-642-744D-28

Sequence: 1 KMLRRIRKIHIIKKXGPTLRIRIRIG 29

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|-------------|---------------------|
| 1 | 103 | 72.5 | 160 | SCS1_SHEEP | P49928 ovine aries |
| 2 | 103 | 72.5 | 160 | SCS2_SHEEP | P49929 ovine aries |
| 3 | 67 | 47.2 | 159 | MB28_BOVIN | P54229 bovis taurus |
| 4 | 57.5 | 40.5 | 178 | Y005_CORGL | O8nnd4 corynebacte |
| 5 | 56.5 | 39.8 | 152 | ARCR_THEMEA | O9kxw9 thermotoga |
| 6 | 54.5 | 38.4 | 152 | O9KXZ0 | O9kxw9 thermotoga |
| 7 | 54 | 38.0 | 146 | O9ALH3 | O9aah3 carsonella |
| 8 | 53 | 37.3 | 138 | R111_ARATH | P56802 arabidopsis |
| 9 | 53 | 37.3 | 138 | O7YJUS | O7YJUS calycanthus |
| 10 | 53 | 37.3 | 196 | O81BES | O81bes bacillus ce |
| 11 | 53 | 37.3 | 308 | O8R2C7 | O8r2c7 mus musculu |
| 12 | 53 | 37.3 | 413 | O6LFRJ3 | O6lfrj3 plasmodium |
| 13 | 52.5 | 37.0 | 140 | O7PDS0 | O7pds0 plasmodium |
| 14 | 52.5 | 37.0 | 193 | O7PDS0 | O7pds0 plasmodium |
| 15 | 52 | 36.6 | 255 | Y005_COREF | O8fuj3 corynebacte |
| 16 | 52 | 36.6 | 255 | O9LFW2 | O9lfw2 arabidopsis |
| 17 | 52 | 36.6 | 267 | O8U1B12 | O8u1b12 plasmodium |
| 18 | 51 | 35.9 | 295 | O8NPH7 | O8nph7 pyrococcus |
| 19 | 51 | 35.9 | 328 | O8NPH7 | O8nph7 pyrococcus |
| 20 | 51 | 35.9 | 467 | O8NPH7 | O8nph7 pyrococcus |
| 21 | 51 | 35.9 | 467 | O8NPH7 | O8nph7 pyrococcus |
| 22 | 51 | 35.9 | 467 | O8NPH7 | O8nph7 pyrococcus |
| 23 | 51 | 35.9 | 467 | O8NPH7 | O8nph7 pyrococcus |
| 24 | 51 | 35.9 | 467 | O8NPH7 | O8nph7 pyrococcus |
| 25 | 50 | 35.2 | 286 | O6LFR79 | O6lfr79 rattus norv |
| 26 | 50 | 35.2 | 297 | O6LFR79 | O6lfr79 rattus norv |
| 27 | 50 | 35.2 | 302 | O6LFR79 | O6lfr79 rattus norv |
| 28 | 50 | 35.2 | 305 | O6LFR79 | O6lfr79 rattus norv |
| 29 | 50 | 35.2 | 305 | O6LFR79 | O6lfr79 rattus norv |
| 30 | 50 | 35.2 | 305 | O6LFR79 | O6lfr79 rattus norv |
| 31 | 50 | 35.2 | 305 | O6LFR79 | O6lfr79 rattus norv |

| | | | | | | |
|----|------|------|------|---|------------|--------------------|
| 32 | 50 | 35.2 | 1730 | 2 | O7RNV8 | O7rnv8 plasmodium |
| 33 | 50 | 35.2 | 1903 | 2 | O9U5D6 | O9u5d6 plautia sta |
| 34 | 50 | 35.2 | 2228 | 2 | O7R123 | O7r123 plasmodium |
| 35 | 49.5 | 34.9 | 448 | 2 | O44570 | O44570 caenorhabdi |
| 36 | 49 | 34.5 | 138 | 1 | R111_LORVA | O9bbq3 lotus japon |
| 37 | 49 | 34.5 | 266 | 2 | O9V0N2 | O9v0n2 pyrococcus |
| 38 | 49 | 34.5 | 363 | 2 | O9UWQ2 | O9uwq2 pyrococcus |
| 39 | 49 | 34.5 | 372 | 2 | O7RUL3 | O7rul3 plasmodium |
| 40 | 49 | 34.5 | 429 | 2 | O97VQ9 | O97vq9 sulfolobus |
| 41 | 49 | 34.5 | 500 | 1 | TF3B_SCHPO | O9p60 schizosacch |
| 42 | 49 | 34.5 | 520 | 1 | O8B8H1 | O8b8h1 pseudomonas |
| 43 | 49 | 34.5 | 734 | 2 | O7RGR5 | O7rgr5 plasmodium |
| 44 | 49 | 34.5 | 807 | 1 | HIS8_PHOHL | O7n611 photorhabdu |
| 45 | 49 | 34.5 | 835 | 2 | O7RNB0 | O7rnb0 plasmodium |

ALIGNMENTS

| RESULT 1 | SCS1_SHEEP | STANDARD | PRT | 160 AA. |
|----------|--|----------|-----|---------|
| ID | SCS1_SHEEP | | | |
| AC | P49928; | | | |
| DT | 01-OCT-1996 (Rel. 34, Created) | | | |
| DT | 01-OCT-1996 (Rel. 34, Last sequence update) | | | |
| DT | 25-OCT-2004 (Rel. 45, Last annotation update) | | | |
| DE | Cathelin-related peptide SCS precursor 1 (Antibacterial peptide SWAP-29) | | | |
| DE | 29) (Myeloid antibacterial peptide SWAP-29). | | | |
| OC | Ovis aries (Sheep). | | | |
| OC | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; | | | |
| OC | Caprinae; Ovis. | | | |
| OK | NCBI_TaxID=9940; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | TISSUE=Bone marrow; | | | |
| RX | MEDLINE=96140581; PubMed=8549789; DOI=10.1016/0014-5793(95)01390-3; | | | |
| RA | Maehoney M.M., Lee A.Y., Brezinski-Caliguri D.J., Huttner K.M.; | | | |
| RT | "Molecular analysis of the sheep cathelin family reveals a novel | | | |
| RT | antimicrobial peptide."; | | | |
| RT | FEBS Lett. 377:519-522(1995). | | | |
| RN | [2] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | TISSUE=Liver; | | | |
| RA | Huttner K.M., Maehoney M.M.; | | | |
| RT | Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases. | | | |
| CC | -1- FUNCTION: Thermostable, broad spectrum, bactericidal agent. | | | |
| CC | -1- SUBCELLULAR LOCATION: Secreted. | | | |
| CC | -1- SIMILARITY: Belongs to the cathelicidin family. | | | |
| CC | This SWISS-PROT entry is copyright. It is produced through a collaboration | | | |
| CC | between the Swiss Institute of Bioinformatics and the EMBL outstation - | | | |
| CC | the European Bioinformatics Institute. There are no restrictions on its | | | |
| CC | use by non-profit institutions as long as its content is in no way | | | |
| CC | modified and this statement is not removed. Usage by and for commercial | | | |
| CC | entities requires a license agreement (See http://www.isb-sib.ch/announce/ | | | |
| CC | or send an email to license@isb-sib.ch). | | | |
| CC | ----- | | | |
| DR | EMBL; X92757; CAA63412.1; - | | | |
| DR | EMBL; U60600; AAB49715.1; - | | | |
| DR | PDB; 1FRY; NMR; A=132-160. | | | |
| DR | InterPro: IPR001894; Cathelicidin. | | | |
| DR | Pfam; PF00666; Cathelicidins; 1. | | | |
| DR | ProDom; PD001838; Cathelicidin; 1. | | | |
| DR | PROSITE; PS00946; CATHELICIDINS_1; 1. | | | |
| DR | PROSITE; PS00947; CATHELICIDINS_2; 1. | | | |
| KW | 3D-structure; Antibiotic; Pyrocidone carboxylic acid; Signal. | | | |
| FT | SIGNAL | 1 | 29 | |
| FT | PROPEP | 30 | 131 | |
| FT | PEPTIDE | 132 | 160 | |
| FT | MOD_RES | 30 | 30 | |
| FT | DISULFID | 86 | 97 | |

By similarity.
Cathelin-related peptide SCS.
Pyrocidone carboxylic acid (by similarity).
By similarity.

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:17:06 ; Search time 53.0419 Seconds
(without alignments)
164.122 Million cell updates/sec

Title: US-09-642-744D-26

Perfect score: 81

Sequence: 1 KIKKELKIKGKIGKLL 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1613378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 74 | 91.4 | 171 | 1 | CP18_RABIT |
| 2 | 56 | 69.1 | 173 | 1 | GRAM_MOUSE |
| 3 | 54 | 66.7 | 1123 | 2 | 068255 |
| 4 | 52 | 64.2 | 170 | 2 | 09GLV5 |
| 5 | 51 | 63.0 | 366 | 2 | 08VQ90 |
| 6 | 49 | 60.5 | 117 | 1 | PFDB_PYRFU |
| 7 | 49 | 60.5 | 170 | 1 | YF59_METUA |
| 8 | 49 | 60.5 | 171 | 2 | 07IKM5 |
| 9 | 49 | 60.5 | 186 | 2 | P70800 |
| 10 | 48 | 59.3 | 117 | 1 | PFDB_PYRAB |
| 11 | 48 | 59.3 | 117 | 1 | PFDB_PYRHO |
| 12 | 48 | 59.3 | 123 | 2 | 09NHL6 |
| 13 | 48 | 59.3 | 324 | 2 | 042621 |
| 14 | 48 | 59.3 | 326 | 2 | 042622 |
| 15 | 48 | 59.3 | 326 | 2 | 042622 |
| 16 | 48 | 59.3 | 1156 | 2 | 066878 |
| 17 | 47 | 58.0 | 68 | 2 | 0970H2 |
| 18 | 47 | 58.0 | 179 | 2 | 06UIV5 |
| 19 | 47 | 58.0 | 179 | 2 | 06UIV7 |
| 20 | 47 | 58.0 | 183 | 2 | 07VCL9 |
| 21 | 47 | 58.0 | 224 | 2 | 09S0D9 |
| 22 | 47 | 58.0 | 244 | 2 | 087584 |
| 23 | 47 | 58.0 | 281 | 2 | 08C8N3 |
| 24 | 47 | 58.0 | 366 | 2 | 08VQ88 |
| 25 | 46 | 56.8 | 124 | 2 | 084W15 |
| 26 | 46 | 56.8 | 124 | 2 | 09FMA8 |
| 27 | 46 | 56.8 | 191 | 2 | 044867 |
| 28 | 46 | 56.8 | 227 | 2 | 045026 |
| 29 | 46 | 56.8 | 284 | 2 | 094B45 |
| 30 | 46 | 56.8 | 343 | 2 | 087302 |
| 31 | 46 | 56.8 | 363 | 2 | 007495 |

ALIGNMENTS

| RESULT 1 | CP18_RABIT | STANDARD: | PRT: | 171 AA. |
|----------|--|-----------|------|---------|
| ID | CP18_RABIT | | | |
| AC | P25230; | | | |
| DT | 01-MAY-1992 (Rel. 22, Created) | | | |
| DT | 01-MAY-1992 (Rel. 22, Last sequence update) | | | |
| DT | 25-OCT-2004 (Rel. 45, Last annotation update) | | | |
| DE | Antimicrobial protein CAP18 precursor (18 kDa lipopolysaccharide-binding protein) (18 kDa cationic protein) (CAP18-A). | | | |
| GN | Name=CAP18; | | | |
| OS | Oryctolagus cuniculus (Rabbit). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus. | | | |
| OX | NCBI_TaxID=9986; | | | |
| RI | (1) | | | |
| RP | SEQUENCE FROM N.A., AND SEQUENCE OF 135-159. | | | |
| RC | TISSUE=Bone marrow; | | | |
| RX | MEDLINE=91354246; PubMed=1883348; | | | |
| RA | Larrick J.W., Morgan J.G., Palings I., Hirata M., Yen M.H.; | | | |
| RT | "Complementary DNA sequence of rabbit CAP18 -- a unique | | | |
| RL | lipopolysaccharide binding protein."; | | | |
| RL | Biochem. Biophys. Res. Commun. 179:170-175(1991). | | | |
| RI | (2) | | | |
| RP | SEQUENCE OF 135-159, AND CHARACTERIZATION. | | | |
| RX | MEDLINE=94178952; PubMed=8132348; | | | |
| RA | Hirata M., Shimomura Y., Yoshida M., Morgan J.G., Palings I., | | | |
| RT | Wilson D., Yen M.H., Wright S.C., Larrick J.W.; | | | |
| RL | "Characterization of a rabbit cationic protein (CAP18) with | | | |
| RL | lipopolysaccharide-inhibitory activity."; | | | |
| RL | Infect. Immun. 62:1421-1426(1994). | | | |
| RI | (3) | | | |
| RP | SEQUENCE OF 135-154, AND CHARACTERIZATION. | | | |
| RX | MEDLINE=94075827; PubMed=8254193; | | | |
| RA | Larrick J.W., Hirata M., Zheng H., Zhong J., Bolin D., | | | |
| RT | Cavallion J.M., Warren H.S., Wright S.C.; | | | |
| RL | "A novel granulocyte-derived peptide with lipopolysaccharide- | | | |
| RL | neutralizing activity."; | | | |
| RL | J. Immunol. 152:231-240(1994). | | | |
| RI | (4) | | | |
| RP | CHARACTERIZATION. | | | |
| RX | MEDLINE=94148064; PubMed=8313956; DOI=10.1016/0014-5793(94)80395-1; | | | |
| RA | Tossi A., Scocchi M., Skerlavaj B., Gennaro R.; | | | |
| RT | "Identification and characterization of a primary antibacterial domain | | | |
| RL | in CAP18, a lipopolysaccharide binding protein from rabbit | | | |
| RL | leukocytes."; | | | |
| RL | FEBS Lett. 339:108-112(1994). | | | |
| RI | (5) | | | |
| RP | STRUCTURE BY NMR OF 135-166. | | | |
| RX | MEDLINE=95377455; PubMed=7649303; DOI=10.1016/0014-5793(95)00792-0; | | | |
| RA | Chen C., Brock R., Luh F., Chou P.-J., Larrick J.W., Huang R.-F., | | | |
| RT | Huang T.-H.; | | | |
| RL | "The solution structure of the active domain of CAP18 -- a | | | |
| RL | lipopolysaccharide binding protein from rabbit leukocytes."; | | | |
| RL | FEBS Lett. 370:46-52(1995). | | | |

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| 32 | 46 | 56.8 | 392 | 2 | 065549 | 065549 arabidopsis |
| 33 | 46 | 56.8 | 405 | 2 | 08VYD9 | 08VYD9 arabidopsis |
| 34 | 46 | 56.8 | 425 | 2 | 09EZI8 | 09EZI8 borrelia bu |
| 35 | 46 | 56.8 | 430 | 2 | 050976 | 050976 borrelia bu |
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| 37 | 46 | 56.8 | 441 | 2 | 09S038 | 09S038 borrelia bu |
| 38 | 46 | 56.8 | 441 | 2 | 09S0B0 | 09S0B0 borrelia bu |
| 39 | 46 | 56.8 | 441 | 2 | 09S0E3 | 09S0E3 borrelia bu |
| 40 | 46 | 56.8 | 441 | 2 | 09S0J4 | 09S0J4 borrelia bu |
| 41 | 46 | 56.8 | 455 | 2 | 09RZY6 | 09RZY6 borrelia bu |
| 42 | 46 | 56.8 | 455 | 2 | 09S076 | 09S076 borrelia bu |
| 43 | 46 | 56.8 | 455 | 2 | 09S0H1 | 09S0H1 borrelia bu |
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| 45 | 46 | 56.8 | 889 | 2 | 08XMY3 | 08XMY3 arabidopsis |
| | | | | | | 08XMY3 clostridium |

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:18:40 / Search time 14.2458 Seconds
(without alignments)
78.601 Million cell updates/sec

Title: US-09-642-744D-24
Perfect score: 75
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Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

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1: Issued Patents AA:
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 75 | 100.0 | 29 | 1 | US-08-313-681A-7 |
| 2 | 75 | 100.0 | 29 | 3 | US-09-322-911-7 |
| 3 | 75 | 100.0 | 171 | 1 | US-08-313-681A-4 |
| 4 | 75 | 100.0 | 171 | 3 | US-09-322-911-4 |
| 5 | 51 | 68.0 | 16 | 1 | US-08-313-681A-11 |
| 6 | 51 | 68.0 | 16 | 3 | US-09-322-911-11 |
| 7 | 47 | 62.7 | 18 | 4 | US-09-525-269A-10 |
| 8 | 46 | 61.3 | 33 | 5 | PCT-US95-12080-4 |
| 9 | 45 | 61.3 | 3421 | 4 | US-09-452-638-53 |
| 10 | 45 | 60.0 | 429 | 4 | US-09-583-110-4660 |
| 11 | 45 | 60.0 | 531 | 4 | US-09-107-433-5016 |
| 12 | 45 | 60.0 | 726 | 4 | US-09-252-991A-26767 |
| 13 | 43 | 57.3 | 693 | 4 | US-09-489-039A-8763 |
| 14 | 42 | 56.0 | 408 | 4 | US-09-248-796A-15721 |
| 15 | 42 | 56.0 | 415 | 4 | US-09-488-039A-13974 |
| 16 | 41 | 54.7 | 452 | 4 | US-09-889-738-21 |
| 17 | 41 | 54.7 | 476 | 4 | US-09-543-681A-7117 |
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| 19 | 40 | 53.3 | 319 | 4 | US-09-252-991A-30168 |
| 20 | 40 | 53.3 | 325 | 4 | US-09-735-846-25 |
| 21 | 40 | 53.3 | 343 | 2 | US-08-559-171A-28 |
| 22 | 40 | 53.3 | 343 | 2 | US-08-646-590B-28 |
| 23 | 40 | 53.3 | 343 | 3 | US-09-069-226-28 |
| 24 | 40 | 53.3 | 343 | 3 | US-09-412-184-28 |
| 25 | 40 | 53.3 | 524 | 4 | US-09-248-796A-18625 |
| 26 | 40 | 53.3 | 898 | 4 | US-09-585-858-37 |
| 27 | 40 | 53.3 | 898 | 4 | US-10-270-878-37 |

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| 28 | 40 | 53.3 | 956 | 4 | US-09-107-532A-5007 | Sequence 5007, Ap |
| 29 | 39 | 52.0 | 18 | 1 | US-07-725-331-28 | Sequence 29, Appl |
| 30 | 39 | 52.0 | 18 | 5 | PCT-US91-05047-29 | Sequence 29, Appl |
| 31 | 39 | 52.0 | 74 | 4 | US-09-248-796A-25957 | Sequence 25957, A |
| 32 | 39 | 52.0 | 87 | 4 | US-09-248-796A-24551 | Sequence 24551, A |
| 33 | 39 | 52.0 | 96 | 4 | US-09-732-210-707 | Sequence 707, App |
| 34 | 39 | 52.0 | 154 | 4 | US-09-248-796A-27970 | Sequence 27970, A |
| 35 | 39 | 52.0 | 166 | 4 | US-09-270-767-36279 | Sequence 36279, A |
| 36 | 39 | 52.0 | 166 | 4 | US-09-270-767-51496 | Sequence 51496, A |
| 37 | 39 | 52.0 | 231 | 4 | US-09-248-796A-14758 | Sequence 14758, A |
| 38 | 39 | 52.0 | 306 | 3 | US-09-134-001C-4678 | Sequence 4678, Ap |
| 39 | 39 | 52.0 | 378 | 4 | US-09-498-520A-44 | Sequence 3723, Ap |
| 40 | 39 | 52.0 | 395 | 3 | US-09-134-001C-3723 | Sequence 3723, Ap |
| 41 | 39 | 52.0 | 396 | 4 | US-09-902-540-15124 | Sequence 15124, A |
| 42 | 39 | 52.0 | 672 | 3 | US-09-040-843-4 | Sequence 4, Appl |
| 43 | 39 | 52.0 | 672 | 3 | US-09-621-855-4 | Sequence 4, Appl |
| 44 | 39 | 52.0 | 817 | 4 | US-09-710-279-50 | Sequence 50, Appl |
| 45 | 39 | 52.0 | 817 | 4 | US-09-710-279-1528 | Sequence 1528, Ap |

ALIGNMENTS

RESULT 1
US-08-313-681A-7
Sequence 7, Application US/08313681A
Patent No. 5618675
GENERAL INFORMATION:
APPLICANT: Larick, James W.
APPLICANT: Wright, Susan C.
APPLICANT: Hiraoka, Mubumasa
TITLE OF INVENTION: Human Cationic Proteins Having
TITLE OF INVENTION: Lipopolysaccharide Binding and Anti-Coagulant Activity
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,681A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15325-9-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2422
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: peptide
FEATURE:
NAME/KEY: Region
LOCATION: 23
OTHER INFORMATION: /note= "Xaa is Asp or Lys"
FEATURE:
NAME/KEY: Region
LOCATION: 26
OTHER INFORMATION: /note= "Xaa is a Gln or Ile"

Tue May 3 11:58:24 2005

US-09-642-744d-24.ral

Pl. mail w/ Office Am
Page 2

NAME/KEY: Region
LOCATION: 27
OTHER INFORMATION: /note= "Xaa is a Gly or Gln"
US-08-313-681A-7

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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRNRKIKKKKIG 15
DB 7 RKRNRKIKKKKIG 21

RESULT 2 *

US-09-322-911-7
Sequence 7, Application US/09322911
Patent No. 6103888

GENERAL INFORMATION:
APPLICANT: Larrick, James W.

APPLICANT: Wright, Susan C.

APPLICANT: Hirata, Mishinaka

APPLICANT: Ballint, Robert F.

TITLE OF INVENTION: Human Cationic Proteins Having

TITLE OF INVENTION: Lipopolysaccharide Binding and Anti-Coagulant Activity

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/322,911

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/691,280

FILING DATE: August 1, 1996

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/916,761

FILING DATE: July 17, 1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/916,765

FILING DATE: July 17, 1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06731

FILING DATE: July 15, 1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/313,681

FILING DATE: September 27, 1994

ATTORNEY/AGENT INFORMATION:
NAME: Fitch, Renee A.

REGISTRATION NUMBER: 35,136

REFERENCE/DOCKET NUMBER: 15325-000920

TELEPHONE: 415-326-2400

TELEFAX: 415-326-2422

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 29 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURES:

NAME/KEY: Region

LOCATION: 23
OTHER INFORMATION: /note= "Xaa is Asp or Lys"

FEATURES:

NAME/KEY: Region

LOCATION: 26

OTHER INFORMATION: /note= "Xaa is a Gln or Ile"

FEATURES:

NAME/KEY: Region

LOCATION: 27

OTHER INFORMATION: /note= "Xaa is a Gly or Gln"

US-09-322-911-7

Query Match: 100.0%; Score 75; DB 3; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.00039;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRNRKIKKKKIG 15
DB 7 RKRNRKIKKKKIG 21

RESULT 3

US-08-313-681A-4

Sequence 4, Application US/08313681A

Patent No. 5618675

GENERAL INFORMATION:
APPLICANT: Larrick, James W.

APPLICANT: Wright, Susan C.

APPLICANT: Hirata, Mishinaka

APPLICANT: Ballint, Robert F.

TITLE OF INVENTION: Human Cationic Proteins Having

TITLE OF INVENTION: Lipopolysaccharide Binding and Anti-Coagulant Activity

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew

STREET: One Market Plaza, Stewart Tower, Suite 2000

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94105

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,681A

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Heelin, James W.

REGISTRATION NUMBER: 29,541

REFERENCE/DOCKET NUMBER: 15325-9-1

TELEPHONE: 415-326-2400

TELEFAX: 415-326-2422

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 171 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-313-681A-4

Query Match: 100.0%; Score 75; DB 1; Length 171;
Best Local Similarity 100.0%; Pred. No. 0.002; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0;

QY 1 RKRNRKIKKKKIG 15
DB 141 RKRNRKIKKKKIG 155

RESULT 4
US-09-322-911-4
Sequence 4, Application US/09322911
Patent No. 610388
GENERAL INFORMATION:
APPLICANT: Larrick, James W.
APPLICANT: Wright, Susan C.
APPLICANT: Hirata, Mishimasa
APPLICANT: Balint, Robert F.
TITLE OF INVENTION: Human Cationic Proteins Having
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/322,911
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/691,280
FILING DATE: August 1, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/916,761
FILING DATE: July 17, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/916,765
FILING DATE: July 17, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06731
FILING DATE: July 15, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/313,681
FILING DATE: September 27, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Flets, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 15325-000920
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 171 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-322-911-4

Query Match 100.0%; Score 75; DB 3; Length 171;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRFRNKIKERLKKIG 15
DB 141 RKRFRNKIKERLKKIG 155

RESULT 5
US-08-313-681A-11
Sequence 11, Application US/08313681A
Patent No. 5618675
GENERAL INFORMATION:

APPLICANT: Larrick, James W.
APPLICANT: Wright, Susan C.
APPLICANT: Hirata, Mishimasa
TITLE OF INVENTION: Human Cationic Proteins Having
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,681A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Healin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15325-9-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-313-681A-11

Query Match 68.0%; Score 51; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.5;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRFRNKIKER 10
DB 7 RKRFRNKIKER 16

RESULT 6
US-09-322-911-11
Sequence 11, Application US/09322911
Patent No. 610388
GENERAL INFORMATION:
APPLICANT: Larrick, James W.
APPLICANT: Wright, Susan C.
APPLICANT: Hirata, Mishimasa
APPLICANT: Balint, Robert F.
TITLE OF INVENTION: Human Cationic Proteins Having
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/322,911

Tue May 3 11:58:24 2005

us-09-642-744d-24.ra1

Pl. mail of office letter
Page 4

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/691,280
FILING DATE: August 1, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/916,761
FILING DATE: July 17, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/916,765
FILING DATE: July 17, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06731
FILING DATE: July 15, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/313,681
FILING DATE: September 27, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Pitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 15325-000920
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-322-911-11

Query Match 68.0%; Score 51; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.5;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKFRNKIKK 10
DB 7 RKFRNKIKK 16

RESULT 7
US-09-525-269A-10
Sequence 10, Application US/09525269A
Patent No. 6743769
GENERAL INFORMATION:
APPLICANT: Yeaman, Michael R.
TITLE OF INVENTION: Antimicrobial Peptides and Derived
FILE REFERENCE: 66742-025(HR5614)
CURRENT APPLICATION NUMBER: US/09/525,269A
CURRENT FILING DATE: 2000-03-13
PRIOR APPLICATION NUMBER: US 09/025,319
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 10
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Antimicrobial peptide designed in part upon
OTHER INFORMATION: microbial domains from platelet microbial
OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
US-09-525-269A-10

Query Match 62.7%; Score 47; DB 4; Length 18;
Best Local Similarity 46.7%; Pred. No. 2;
Matches 7; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
QY 1 RKFRNKIKKIKG 15

DB 4 KKKKKKKKKIKG 18

RESULT 8
PCT-US95-12080-4
Sequence 4, Application PC/TUS9512080
GENERAL INFORMATION:
APPLICANT: Children's Medical Center Corporation
TITLE OF INVENTION: Synuclein Mediated Modulation of Tissue Repair
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/12080
FILING DATE:
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-873-8794
TELEFAX: (404)-815-8795
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US95-12080-4

Query Match 61.3%; Score 46; DB 5; Length 33;
Best Local Similarity 73.3%; Pred. No. 4.8;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 RKFRNKIKKIKG 15
DB 4 KKKKKKKKKIKG 18

RESULT 9
US-09-452-638-53
Sequence 53, Application US/09452638
Patent No. 6696281
GENERAL INFORMATION:
APPLICANT: Chambers, Thomas J.
APPLICANT: Monath, Thomas P.
TITLE OF INVENTION: Chimeric Flavivirus Vaccines
FILE REFERENCE: 06132/033004
CURRENT APPLICATION NUMBER: US/09/452,638
CURRENT FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: US 09/121,587
PRIOR FILING DATE: 1998-07-23
PRIOR APPLICATION NUMBER: PCT/US98/03894
PRIOR FILING DATE: 1998-03-02
PRIOR APPLICATION NUMBER: US 09/007,664
PRIOR FILING DATE: 1998-01-15
PRIOR APPLICATION NUMBER: US 08/807,445
PRIOR FILING DATE: 1997-02-28
NUMBER OF SEQ ID NOS: 85
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 53
LENGTH: 3421
TYPE: PRT
ORGANISM: Artificial Sequence

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:18:40 ; Search time 17.095 Seconds

(without alignments)
78.601 Million cell updates/sec

Title: US-09-642-744D-20

Sequence: 1 KRLKRPKIKIKKIKIG 18

Scoring table: BLOSUM62

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Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 1 | 89 | 100.0 | 29 | 1 | US-08-313-681A-7 |
| 2 | 89 | 100.0 | 29 | 3 | US-09-322-911-7 |
| 3 | 89 | 100.0 | 171 | 1 | US-08-313-681A-4 |
| 4 | 89 | 100.0 | 171 | 3 | US-09-322-911-4 |
| 5 | 65 | 73.0 | 16 | 1 | US-08-313-681A-11 |
| 6 | 65 | 73.0 | 16 | 3 | US-09-322-911-11 |
| 7 | 50 | 56.2 | 33 | 5 | PCT-US95-12080-4 |
| 8 | 50 | 56.2 | 258 | 4 | US-09-828-4447-13 |
| 9 | 49 | 55.1 | 18 | 4 | US-09-525-269A-10 |
| 10 | 49 | 55.1 | 326 | 4 | US-09-735-846-25 |
| 11 | 49 | 55.1 | 452 | 4 | US-09-889-738-21 |
| 12 | 47 | 52.8 | 3421 | 4 | US-07-452-638-53 |
| 13 | 46 | 51.7 | 18 | 1 | US-07-725-331-29 |
| 14 | 46 | 51.7 | 18 | 5 | PCT-US91-05047-29 |
| 15 | 46 | 51.7 | 123 | 4 | US-09-148-545-187 |
| 16 | 46 | 51.7 | 123 | 4 | US-09-148-545-243 |
| 17 | 46 | 51.7 | 188 | 4 | US-09-695-795A-6 |
| 18 | 46 | 51.7 | 329 | 4 | US-09-735-846-24 |
| 19 | 46 | 51.7 | 331 | 4 | US-09-735-846-23 |
| 20 | 45 | 50.6 | 223 | 4 | US-09-344-624-12 |
| 21 | 45 | 50.6 | 269 | 4 | US-09-744-989C-3 |
| 22 | 45 | 50.6 | 287 | 4 | US-09-744-989C-1 |
| 23 | 45 | 50.6 | 287 | 4 | US-09-744-989C-5 |
| 24 | 45 | 50.6 | 429 | 4 | US-09-583-110-4660 |
| 25 | 45 | 50.6 | 531 | 4 | US-09-107-433-5016 |
| 26 | 45 | 50.6 | 726 | 4 | US-09-253-991A-26767 |
| 27 | 45 | 50.6 | 1244 | 4 | US-09-949-016-11702 |

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| 28 | 44 | 49.4 | 96 | 4 | US-09-732-210-707 | Sequence 707, App |
| 29 | 44 | 49.4 | 103 | 3 | US-09-308-388-1 | Sequence 1, Appl |
| 30 | 44 | 49.4 | 187 | 3 | US-08-493-071-16 | Sequence 16, Appl |
| 31 | 44 | 49.4 | 236 | 3 | US-08-493-071-15 | Sequence 15, Appl |
| 32 | 44 | 49.4 | 277 | 1 | US-08-690-457-5 | Sequence 5, Appl |
| 33 | 44 | 49.4 | 277 | 2 | US-08-628-187-5 | Sequence 5, Appl |
| 34 | 44 | 49.4 | 277 | 3 | US-08-493-071-3 | Sequence 3, Appl |
| 35 | 44 | 49.4 | 287 | 1 | US-08-690-457-4 | Sequence 4, Appl |
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| 37 | 44 | 49.4 | 287 | 3 | US-08-493-071-2 | Sequence 2, Appl |
| 38 | 44 | 49.4 | 288 | 1 | US-08-690-457-3 | Sequence 3, Appl |
| 39 | 44 | 49.4 | 288 | 2 | US-08-628-187-3 | Sequence 3, Appl |
| 40 | 44 | 49.4 | 288 | 3 | US-08-493-071-1 | Sequence 1, Appl |
| 41 | 43 | 48.3 | 18 | 1 | US-07-725-331-24 | Sequence 24, Appl |
| 42 | 43 | 48.3 | 18 | 1 | US-07-725-331-27 | Sequence 27, Appl |
| 43 | 43 | 48.3 | 18 | 5 | PCT-US91-05047-24 | Sequence 24, Appl |
| 44 | 43 | 48.3 | 18 | 5 | PCT-US91-05047-27 | Sequence 27, Appl |
| 45 | 43 | 48.3 | 158 | 4 | US-09-107-532A-5475 | Sequence 5475, Ap |

ALIGNMENTS

RESULT 1
US-08-313-681A-7
Sequence 7, Application US/08313681A
Patent No. 5618675
GENERAL INFORMATION:
APPLICANT: Larrick, James W.
APPLICANT: Wright, Susan C.
APPLICANT: Hirata, Miehlmasa
TITLE OF INVENTION: Human Cationic Proteins Having
TITLE OF INVENTION: Lipopolysaccharide Binding and Anti-Coagulant Activity
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESSES:
ADDRESSER: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,681A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Heilin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15325-9-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURES:
NAME/KEY: Region
LOCATION: 23
OTHER INFORMATION: /note= "Xaa is Asp or Lys"
NAME/KEY: Region
LOCATION: 26
OTHER INFORMATION: /note= "Xaa is a Gln or Ile"

RESULT 4
US-09-322-911-4
Sequence 4, Application US/09322911
Patent No. 6103888
GENERAL INFORMATION:
APPLICANT: Larrick, James W.
APPLICANT: Wright, Susan C.
APPLICANT: Hiraoka, Mshimasa
APPLICANT: Balint, Robert F.
TITLE OF INVENTION: Human Cationic Proteins Having
Lipopolysaccharide Binding and Anti-Coagulant Activity
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSES: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/322,911
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/691,280
FILING DATE: August 1, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/916,761
FILING DATE: July 17, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/916,765
FILING DATE: July 17, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06731
FILING DATE: July 15, 1993
APPLICATION DATA:
APPLICATION NUMBER: 08/313,681
FILING DATE: September 27, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Fitch, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 15325-000920
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 171 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-322-911-4
Query Match 100.0%; Score 89; DB 3; Length 171;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KRLRKPNNKIKKKIG 18
DB 138 KRLRKPNNKIKKKIG 155
RESULT 5
US-08-313-681A-11
Sequence 11, Application US/08313681A
Patent No. 5618675
GENERAL INFORMATION:

APPLICANT: Larrick, James W.
APPLICANT: Wright, Susan C.
APPLICANT: Hiraoka, Mshimasa
TITLE OF INVENTION: Human Cationic Proteins Having
Lipopolysaccharide Binding and Anti-Coagulant Activity
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSES: Townsend and Townsend and Crew LLP
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,681A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15325-9-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-313-681A-11
Query Match 73.0%; Score 65; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KRLRKPNNKIKKK 13
DB 4 KRLRKPNNKIKKK 16
RESULT 6
US-09-322-911-11
Sequence 11, Application US/09322911
Patent No. 6103888
GENERAL INFORMATION:
APPLICANT: Larrick, James W.
APPLICANT: Wright, Susan C.
APPLICANT: Hiraoka, Mshimasa
APPLICANT: Balint, Robert F.
TITLE OF INVENTION: Human Cationic Proteins Having
Lipopolysaccharide Binding and Anti-Coagulant Activity
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSES: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/322,911

FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/691,280
 FILING DATE: August 1, 1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/916,761
 FILING DATE: July 17, 1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/916,765
 FILING DATE: July 17, 1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US93/06731
 FILING DATE: July 15, 1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/313,681
 FILING DATE: September 27, 1994
 ATTORNEY/AGENT INFORMATION:
 NAME: FITE, Renee A.
 REGISTRATION NUMBER: 35,136
 REFERENCE/DOCKET NUMBER: 15325-000920
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-326-2400
 TELEFAX: 415-326-2422
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 16 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-322-911-11

Query Match 73.0%; Score 65; DB 3; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.019;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KRLRFRNKIKER 13
 DB 4 KRLRFRNKIKER 16

RESULT 7
 PCT-US95-12080-4
 Sequence 4, Application PC/TUS9512080
 GENERAL INFORMATION:
 APPLICANT: Children's Medical Center Corporation
 TITLE OF INVENTION: Synducin Mediated Modulation of Tissue Repair
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSER: Patrea L. Pabst
 STREET: 2800 One Atlantic Center
 CITY: Atlanta
 STATE: Georgia
 COUNTRY: USA
 ZIP: 30309-3450
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/12080
 FILING DATE:
 CLASSIFICATION:
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (404)-873-8794
 TELEFAX: (404)-815-8795
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 33 amino acids
 TYPE: amino acid

TOPOLOGY: linear
 PCT-US95-12080-4

Query Match 56.2%; Score 50; DB 5; Length 33;
 Best Local Similarity 75.0%; Pred. No. 3.4;
 Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 LKFRNKIKERKKG 18
 DB 3 LKRGKIKERKKG 18

RESULT 8
 US-09-828-447-13
 Sequence 13, Application US/09828447
 Patent No. 6720477
 GENERAL INFORMATION:
 APPLICANT: COSTA E SILVA, OSWALDO DA
 APPLICANT: BOHNETT, HANS J.
 APPLICANT: VAN THIELEN, NOCHA
 APPLICANT: CHEN, ROUYING
 APPLICANT: ISHITANI, MANABU
 TITLE OF INVENTION: SIGNAL TRANSDUCTION STRESS-RELATED PROTEINS AND METHODS
 FILE REFERENCE: 16313-0037
 CURRENT APPLICATION NUMBER: US/09/828,447
 PRIOR FILING DATE: 2001-08-20
 PRIOR APPLICATION NUMBER: 60/196,001
 PRIOR FILING DATE: 2000-04-07
 NUMBER OF SEQ ID NOS: 41
 SOFTWARE: Patent In Ver. 2.1
 SEQ ID NO 13
 LENGTH: 258
 TYPE: PRT
 ORGANISM: Physcomitrella patens
 US-09-828-447-13

Query Match 56.2%; Score 50; DB 4; Length 258;
 Best Local Similarity 47.1%; Pred. No. 22;
 Matches 8; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 1 KRLRFRNKIKERKKG 17
 DB 83 KRLRFRNKIKERKKG 99

RESULT 9
 US-09-525-269A-10
 Sequence 10, Application US/09525269A
 Patent No. 6743769
 GENERAL INFORMATION:
 APPLICANT: Yeaman, Michael R.
 APPLICANT: Shen, Alexander J.
 TITLE OF INVENTION: Antimicrobial Peptides and Derived
 FILE REFERENCE: 66742-025(HR5614)
 CURRENT APPLICATION NUMBER: US/09/525,269A
 PRIOR FILING DATE: 2000-03-13
 PRIOR APPLICATION NUMBER: US 09/025,319
 NUMBER OF SEQ ID NOS: 39
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 10
 LENGTH: 18
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Antimicrobial peptide designed in part upon
 OTHER INFORMATION: microbicidal domains from platelet microbial
 OTHER INFORMATION: proteins 1 and 2 (PMP-1 and PMP-2) from rabbits
 US-09-525-269A-10

Query Match 55.1%; Score 49; DB 4; Length 18;

As mail w/ office copy

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RESULT 2
US-09-322-911-4
Sequence 4, Application US/09322911
Patent No. 6103888
GENERAL INFORMATION:
APPLICANT: Latrick, James W.
APPLICANT: Wright, Susan C.
APPLICANT: Hirata, Mshimasa
APPLICANT: Balint, Robert F.
TITLE OF INVENTION: Human Cationic Proteins Having
Lipopolysaccharide Binding and Anti-Coagulant Activity
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/322,911
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/691,280
FILING DATE: August 1, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/916,761
FILING DATE: July 17, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/916,765
FILING DATE: July 17, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06731
FILING DATE: July 15, 1993
APPLICATION DATA:
APPLICATION NUMBER: 08/313,681
FILING DATE: September 27, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Fitch, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 15325-000920
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 171 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-322-911-4

Query Match 100.0%; Score 108; DB 3; Length 171;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 RRLRRFRNKKIKKKIGOKI 22
DB 137 RRLRRFRNKKIKKKIGOKI 158
RESULT 3
US-08-313-681A-7
Sequence 7, Application US/08313681A
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* Patent No. 5618675
GENERAL INFORMATION:
APPLICANT: Latrick, James W.
APPLICANT: Wright, Susan C.
APPLICANT: Hirata, Mshimasa
APPLICANT: Balint, Robert F.
TITLE OF INVENTION: Human Cationic Proteins Having
Lipopolysaccharide Binding and Anti-Coagulant Activity
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,681A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15325-9-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURES:
NAME/KEY: Region
LOCATION: 23
OTHER INFORMATION: /note= "Xaa is Asp or Lys"
FEATURE:
NAME/KEY: Region
LOCATION: 26
OTHER INFORMATION: /note= "Xaa is a Gln or Ile"
FEATURE:
NAME/KEY: Region
LOCATION: 27
OTHER INFORMATION: /note= "Xaa is a Gly or Gln"
US-08-313-681A-7

Query Match 94.4%; Score 102; DB 1; Length 29;
Best Local Similarity 95.5%; Pred. No. 1.5e-06;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DB 3 RRLRRFRNKKIKKKIGOKI 24
RESULT 4
US-09-322-911-7
Sequence 7, Application US/09322911
Patent No. 6103888
GENERAL INFORMATION:
APPLICANT: Latrick, James W.
APPLICANT: Wright, Susan C.
APPLICANT: Hirata, Mshimasa
APPLICANT: Balint, Robert F.
TITLE OF INVENTION: Human Cationic Proteins Having
Lipopolysaccharide Binding and Anti-Coagulant Activity
NUMBER OF SEQUENCES: 30
```

Pls. mail w/ official

Tue May 3 11:58:19 2005

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, 8th Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/322,911
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/691,280
 FILING DATE: August 1, 1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/916,761
 FILING DATE: July 17, 1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/916,765
 FILING DATE: July 17, 1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US93/06731
 FILING DATE: July 15, 1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/313,681
 FILING DATE: September 27, 1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Fitch, Renee A.
 REGISTRATION NUMBER: 35,136
 REFERENCE/DOCKET NUMBER: 15325-000920
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-326-2400
 TELEFAX: 415-326-2422
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 29 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FEATURES:
 NAME/KEY: Region
 LOCATION: 23
 OTHER INFORMATION: /note= "Xaa is Asp or Lys"
 FEATURE:
 NAME/KEY: Region
 LOCATION: 26
 OTHER INFORMATION: /note= "Xaa is a Gln or Ile"
 FEATURE:
 NAME/KEY: Region
 LOCATION: 27
 OTHER INFORMATION: /note= "Xaa is a Gly or Gln"
 US-09-322-911-7
 Query Match 94.4%; Score 102; DB 3; Length 29;
 Best Local Similarity 95.5%; Pred. No. 1.5e-06;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RKRLKPKFKIKKIGOKI 22
 DB 3 RKRLKPKFKIKKIGOKI 24
 RESULT 5
 US-08-313-681A-11
 Sequence 11, Application US/08313681A
 Patent No. 5618675
 GENERAL INFORMATION:

APPLICANT: Larrick, James W.
 APPLICANT: Wright, Susan C.
 APPLICANT: Hirata, Mishimasa
 TITLE OF INVENTION: Human Cationic Proteins Having
 TITLE OF INVENTION: Lipopolysaccharide Binding and Anti-Coagulant Activity
 NUMBER OF SEQUENCES: 30
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: One Market Plaza, Steuart Tower, Suite 2000
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94105
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/313,681A
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Healin, James M.
 REGISTRATION NUMBER: 29,541
 REFERENCE/DOCKET NUMBER: 15325-9-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-326-2400
 TELEFAX: 415-326-2422
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 16 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-313-681A-11
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 Best Local Similarity 100.0%; Pred. No. 0.0092;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RKRLKPKFKIKK 14
 DB 3 RKRLKPKFKIKK 16
 RESULT 6
 US-09-322-911-11
 Sequence 11, Application US/09322911
 Patent No. 610388
 GENERAL INFORMATION:
 APPLICANT: Larrick, James W.
 APPLICANT: Wright, Susan C.
 APPLICANT: Hirata, Mishimasa
 APPLICANT: Balint, Robert F.
 TITLE OF INVENTION: Human Cationic Proteins Having
 TITLE OF INVENTION: Lipopolysaccharide Binding and Anti-Coagulant Activity
 NUMBER OF SEQUENCES: 30
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, 8th Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/322,911

Please mail at office door

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/691,280
FILING DATE: August 1, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/916,761
FILING DATE: July 17, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/916,765
FILING DATE: July 17, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06731
FILING DATE: July 15, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/313,681
FILING DATE: September 27, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Fiteb, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 15325-000920
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-322-911-11

Query Match 64.8%; Score 70; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.0092; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRLRRFRNKKIKK 14
Db 3 RRLRRFRNKKIKK 16

RESULT 7
PCT-US95-12080-4
Sequence 4, Application PC/TUS9512080
GENERAL INFORMATION:
APPLICANT: Children's Medical Center Corporation
TITLE OF INVENTION: Synuclein Mediated Modulation of Tissue Repair
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: Patricia L. Pabst
STREET: 2800 One Atlantic Center
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/12080
FILING DATE:
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-873-8794
TELEFAX: (404)-815-8795
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid

TOPOLOGY: linear
PCT-US95-12080-4

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Best Local Similarity 78.9%; Pred. No. 0.1;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 LRKPKKIKKKIKKIGOKI 22
Db 3 LRKPKKIKKKIKKIGOKI 21

RESULT 8
US-09-735-846-25
Sequence 25, Application US/09735846
Patent No. 6730823
GENERAL INFORMATION:
APPLICANT: Allen, Stephen M.
APPLICANT: Kinney, Anthony J.
APPLICANT: Falco, S. Carl
TITLE OF INVENTION: PLANT CHOLINE PHOSPHATE CYTIDYLTRANSFERASE
FILE REFERENCE: BBI419 US NA
CURRENT APPLICATION NUMBER: US/09/735,846
CURRENT FILING DATE: 2000-12-13
PRIOR APPLICATION NUMBER: 60/170,375
PRIOR FILING DATE: 13 DECEMBER 1999
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Microsoft Office 97
SEQ ID NO 25
LENGTH: 326
TYPE: PRT
ORGANISM: Brassica napus
US-09-735-846-25

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Qy 3 RLKPKKIKKKIKKIGOKI 22
Db 198 RLKPKKIKKKIKKIGOKI 217

RESULT 9
US-09-735-846-24
Sequence 24, Application US/09735846
Patent No. 6730823
GENERAL INFORMATION:
APPLICANT: Allen, Stephen M.
APPLICANT: Kinney, Anthony J.
APPLICANT: Falco, S. Carl
TITLE OF INVENTION: PLANT CHOLINE PHOSPHATE CYTIDYLTRANSFERASE
FILE REFERENCE: BBI419 US NA
CURRENT APPLICATION NUMBER: US/09/735,846
CURRENT FILING DATE: 2000-12-13
PRIOR APPLICATION NUMBER: 60/170,375
PRIOR FILING DATE: 13 DECEMBER 1999
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Microsoft Office 97
SEQ ID NO 24
LENGTH: 329
TYPE: PRT
ORGANISM: Brassica napus
US-09-735-846-24

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Matches 9; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

Qy 3 RLKPKKIKKKIKKIGOKI 22
Db 205 RLKPKKIKKKIKKIGOKI 224

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Tue May 3 11:58:15 2005

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 2, 2005, 12:18:40 / Search time 19.9441 Seconds
(without alignments)
78.601 Million cell updates/sec

Title: US-09-642-744D-19

Perfect score: 104

Sequence: 1 GKKRLRKFRNKIKKKKIG 21

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

Issued Patents AA: *
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3: /cgn2_6/ptodata/1/1aa/6A COMB pep: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 3 | 104 | 100.0 | 171 | 1 US-08-313-681A-4 | Sequence 4, Appl1 |
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| 5 | 80 | 76.9 | 16 | 1 US-08-313-681A-11 | Sequence 11, Appl1 |
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| 8 | 50 | 48.1 | 33 | 5 PCT-US95-12080-4 | Sequence 4, Appl1 |
| 9 | 50 | 48.1 | 18 | 4 US-09-828-447-13 | Sequence 13, Appl1 |
| 10 | 49 | 47.1 | 37 | 1 US-09-525-269A-10 | Sequence 10, Appl1 |
| 11 | 49 | 47.1 | 37 | 1 US-08-313-681A-6 | Sequence 6, Appl1 |
| 12 | 49 | 47.1 | 37 | 3 US-09-322-911-6 | Sequence 6, Appl1 |
| 13 | 49 | 47.1 | 245 | 4 US-09-543-681A-6428 | Sequence 6428, Ap |
| 14 | 49 | 47.1 | 269 | 4 US-09-744-989C-3 | Sequence 3, Appl1 |
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| 20 | 48 | 46.2 | 236 | 3 US-09-308-388-1 | Sequence 1, Appl1 |
| 21 | 48 | 46.2 | 277 | 1 US-08-493-071-15 | Sequence 15, Appl1 |
| 22 | 48 | 46.2 | 277 | 1 US-08-628-187-5 | Sequence 5, Appl1 |
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ALIGNMENTS

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| 28 | 48 | 46.2 | 288 | 2 | US-08-628-187-3 | Sequence 3, Appl1 |
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| 32 | 47 | 45.2 | 223 | 4 | US-09-344-624-12 | Sequence 12, Appl1 |
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| 34 | 46 | 44.2 | 18 | 1 | US-07-725-331-29 | Sequence 29, Appl1 |
| 35 | 46 | 44.2 | 18 | 5 | PCT-US91-05047-29 | Sequence 29, Appl1 |
| 36 | 46 | 44.2 | 123 | 4 | US-08-148-545-187 | Sequence 187, App |
| 37 | 46 | 44.2 | 123 | 4 | US-09-148-545-143 | Sequence 243, App |
| 38 | 46 | 44.2 | 188 | 4 | US-09-695-795A-6 | Sequence 6, Appl1 |
| 39 | 46 | 44.2 | 329 | 4 | US-09-735-846-24 | Sequence 24, Appl1 |
| 40 | 46 | 44.2 | 331 | 4 | US-09-735-846-23 | Sequence 23, Appl1 |
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| 43 | 46 | 44.2 | 413 | 4 | US-09-614-069-14 | Sequence 14, Appl1 |
| 44 | 46 | 44.2 | 413 | 4 | US-09-821-803A-7 | Sequence 7, Appl1 |
| 45 | 46 | 44.2 | 413 | 4 | US-09-821-803A-8 | Sequence 8, Appl1 |

RESULT 1
US-08-313-681A-7
Sequence 7, Application US/08313681A
Patent No. 5618675
GENERAL INFORMATION:
APPLICANT: Larrick, James W.
APPLICANT: Wright, Susan C.
APPLICANT: Hirata, Mshimasa
TITLE OF INVENTION: Human Cationic Proteins Having
TITLE OF INVENTION: Lipopolysaccharide Binding and Anti-Coagulant Activity
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,681A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Healin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15325-9-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
FAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURES:
NAME/KEY: Region
LOCATION: 23
OTHER INFORMATION: /note= "Xaa is Asp or Lys"
FEATURE:
NAME/KEY: Region
LOCATION: 26
OTHER INFORMATION: /note= "Xaa is a Gln or Ile"
FEATURE:

NAME/KEY: Region
LOCATION: 27
OTHER INFORMATION: /note="Xaa is a Gly or Gln"
US-08-313-681A-7

Query Match 100.0%; Score 104; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 6.7e-07;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLKRLRFRNKIKKIKKIG 21
DB 1 GLKRLRFRNKIKKIKKIG 21

RESULT 2
US-09-322-911-7
Sequence 7, Application US/09322911
Patent No. 6103888

GENERAL INFORMATION:
APPLICANT: Larrick, James W.
APPLICANT: Wright, Susan C.
APPLICANT: Hirata, Mshimasa
APPLICANT: Balint, Robert P.
TITLE OF INVENTION: Human Cationic Proteins Having
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/322,911
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/691,280

FILING DATE: August 1, 1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/916,761

FILING DATE: July 17, 1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/916,765

FILING DATE: July 17, 1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/06731

FILING DATE: July 15, 1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/313,681

FILING DATE: September 27, 1994

ATTORNEY/AGENT INFORMATION:

NAME: Pitts, Renee A.

REGISTRATION NUMBER: 35,136

REFERENCE/DOCKET NUMBER: 15325-000920

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-326-2400

TELEFAX: 415-326-2422

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 29 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: Region

LOCATION: 23
OTHER INFORMATION: /note="Xaa is Asp or Lys"

FEATURE:

NAME/KEY: Region

LOCATION: 26

OTHER INFORMATION: /note="Xaa is a Gln or Ile"

FEATURE:

NAME/KEY: Region

LOCATION: 27

OTHER INFORMATION: /note="Xaa is a Gly or Gln"

QY 1 GLKRLRFRNKIKKIKKIG 21
DB 1 GLKRLRFRNKIKKIKKIG 21

RESULT 3
US-08-313-681A-4
Sequence 4, Application US/08313681A
Patent No. 5618675

GENERAL INFORMATION:
APPLICANT: Larrick, James W.
APPLICANT: Wright, Susan C.
APPLICANT: Hirata, Mshimasa
TITLE OF INVENTION: Human Cationic Proteins Having
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,681A
FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Heslin, James M.

REGISTRATION NUMBER: 29,541

REFERENCE/DOCKET NUMBER: 15325-9-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-326-2400

TELEFAX: 415-326-2422

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 171 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

FEATURE:

NAME/KEY: Region

US-08-313-681A-4

Query Match 100.0%; Score 104; DB 1; Length 171;
Best Local Similarity 100.0%; Pred. No. 3.5e-06;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLKRLRFRNKIKKIKKIG 21
DB 135 GLKRLRFRNKIKKIKKIG 155

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Pls. mail w/ office letter

RESULT 4

US-09-322-911-4

Sequence 4, Application US/09322911

Patent No. 6103888

GENERAL INFORMATION:

APPLICANT: Larrick, James W.

APPLICANT: Wright, Susan C.

APPLICANT: Hirata, Mishimasa

APPLICANT: Balint, Robert F.

TITLE OF INVENTION: Human Cationic Proteins Having

NUMBER OF SEQUENCES: 30 Lipopolysaccharide Binding and Anti-Coagulant Activity

CORRESPONDENCE ADDRESS:

ADDRESS: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/322,911

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/691,280

FILING DATE: August 1, 1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/916,761

FILING DATE: July 17, 1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/916,765

FILING DATE: July 17, 1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/06731

FILING DATE: July 15, 1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/313,681

FILING DATE: September 27, 1994

ATTORNEY/AGENT INFORMATION:

NAME: Fitts, Renee A.

REGISTRATION NUMBER: 35,136

REFERENCE/DOCKET NUMBER: 15325-000920

TELEPHONE: 415-326-2400

TELEFAX: 415-326-2422

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 171 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-322-911-4

Query Match 100.0%; Score 104; DB 3; Length 171;
Best Local Similarity 100.0%; Pred. No. 3.5e-06;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GRRRLRRFRNKKIKKIG 21
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 135 GRRRLRRFRNKKIKKIG 155

RESULT 5
 US-08-313-681A-11
 Sequence 11, Application US/08313681A
 Patent No. 5618675
 GENERAL INFORMATION:

APPLICANT: Larrick, James W.
 APPLICANT: Wright, Susan C.
 APPLICANT: Hirata, Mishimasa
 APPLICANT: Balint, Robert F.
 TITLE OF INVENTION: Human Cationic Proteins Having
 NUMBER OF SEQUENCES: 30 Lipopolysaccharide Binding and Anti-Coagulant Activity

CORRESPONDENCE ADDRESS:
 ADDRESS: Townsend and Townsend and Crew
 STREET: One Market Plaza, Steuart Tower, Suite 2000
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94105

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/313,681A
 FILING DATE:

CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Heelin, James M.
 REGISTRATION NUMBER: 29,541
 REFERENCE/DOCKET NUMBER: 15325-9-1
 TELEPHONE: 415-326-2400
 TELEFAX: 415-326-2422
 INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:
 LENGTH: 16 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-313-681A-11

Query Match 76.9%; Score 80; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.00042;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GRRRLRRFRNKKIKK 16
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 1 GRRRLRRFRNKKIKK 16

RESULT 6
 US-09-322-911-11
 Sequence 11, Application US/09322911
 Patent No. 6103888

GENERAL INFORMATION:

APPLICANT: Larrick, James W.

APPLICANT: Wright, Susan C.

APPLICANT: Hirata, Mishimasa

APPLICANT: Balint, Robert F.

TITLE OF INVENTION: Human Cationic Proteins Having

NUMBER OF SEQUENCES: 30 Lipopolysaccharide Binding and Anti-Coagulant Activity

CORRESPONDENCE ADDRESS:

ADDRESS: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/322,911

Tue May 3 11:58:15 2005

us-09-642-744d-19.ral

Pls. mail w/ office copy
Page 4

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/691,280
FILING DATE: August 1, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/916,761
FILING DATE: July 17, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/916,765
FILING DATE: July 17, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06731
FILING DATE: July 15, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/313,681
FILING DATE: September 27, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Fiteb, Renee A.
REGISTRATION NUMBER: 35,135
REFERENCE/DOCKET NUMBER: 15325-000920
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-322-911-11

Query Match 76.9%; Score 80; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.00042;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GRRRLRRRNKIKK 16
Db 1 GRRRLRRRNKIKK 16

RESULT 7
US-09-452-638-53
Sequence 53, Application US/09452638
Patent No. 6696281
GENERAL INFORMATION:
APPLICANT: Chambers, Thomas J.
APPLICANT: Monath, Thomas P.
APPLICANT: Gutrahoo, Farshad
TITLE OF INVENTION: Chimeric Flavivirus Vaccines
FILE REFERENCE: 06132/033004
CURRENT APPLICATION NUMBER: US/09/452,638
CURRENT FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: US 09/121,587
PRIOR FILING DATE: 1998-07-23
PRIOR APPLICATION NUMBER: PCT/US98/03894
PRIOR FILING DATE: 1998-03-02
PRIOR APPLICATION NUMBER: US 09/007,664
PRIOR FILING DATE: 1998-01-15
PRIOR APPLICATION NUMBER: US 08/807,445
PRIOR FILING DATE: 1997-02-28
NUMBER OF SEQ ID NOS: 85
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 53
LENGTH: 3421
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: derived from yellow fever virus and Japanese
US-09-452-638-53

Query Match 51.0%; Score 53; DB 4; Length 3421;
Best Local Similarity 50.0%; Pred. No. 1.7e+02;
Matches 10; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
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Db 16 VRRGVRSLSNKIKK 35

RESULT 8
PCT-US95-12080-4
Sequence 4, Application PC/TUS9512080
GENERAL INFORMATION:
APPLICANT: Children's Medical Center Corporation
TITLE OF INVENTION: Synuclein Mediated Modulation of Tissue Repair
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESS: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/12080
FILING DATE:
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-873-8794
TELEFAX: (404)-815-8795
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US95-12080-4

Query Match 48.1%; Score 50; DB 5; Length 33;
Best Local Similarity 75.0%; Pred. No. 5.3;
Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 6 LRRRNKIKK 21
Db 3 LRRGKIKK 18

RESULT 9
US-09-828-447-13
Sequence 13, Application US/09828447
Patent No. 6720477
GENERAL INFORMATION:
APPLICANT: COSTA E SILVA, OSWALDO DA
APPLICANT: BOHNETT, HANS J.
APPLICANT: VAN THIELEN, NOCHA
APPLICANT: CHEN, ROUYING
APPLICANT: ISHITANI, MAMARU
TITLE OF INVENTION: SIGNAL TRANSDUCTION STRESS-RELATED PROTEINS AND METHODS
FILE REFERENCE: 16313-0037
CURRENT APPLICATION NUMBER: US/09/828,447
CURRENT FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: 60/196,001
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 13
LENGTH: 258

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 2, 2005, 13:03:56 ; Search time 78.8994 Seconds

(without alignments)
122.435 Million cell updates/sec

Title: US-09-642-744D-28

Sequence: 1 KNLRRIRKIHIIKKYGPITLIRITIG 29

Scoring table: BLOSUM62

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Searched: 1426032 seqs, 333106140 residues

Total number of hits satisfying chosen parameters: 1426032

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Published Applications AA:*
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2: /cgn2_6/ptodata/1/pubppa/PCR_NEW_PUB.pep:*
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11: /cgn2_6/ptodata/1/pubppa/US09C_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 142 | 100.0 | 29 | 15 US-10-721-839-8 | Sequence 8, Appli |
| 3 | 104 | 73.2 | 21 | 14 US-10-060-102-17 | Sequence 17, Appli |
| 4 | 104 | 73.2 | 21 | 15 US-10-721-839-17 | Sequence 17, Appli |
| 5 | 104 | 73.2 | 23 | 14 US-10-060-102-16 | Sequence 16, Appli |
| 6 | 104 | 73.2 | 23 | 15 US-10-721-839-16 | Sequence 16, Appli |
| 7 | 103 | 72.5 | 29 | 14 US-10-060-102-4 | Sequence 4, Appli |
| 8 | 103 | 72.5 | 29 | 15 US-10-721-839-4 | Sequence 4, Appli |
| 9 | 103 | 72.5 | 160 | 9 US-09-917-340-36 | Sequence 36, Appli |
| 10 | 103 | 72.5 | 160 | 17 US-10-844-837-36 | Sequence 36, Appli |
| 11 | 103 | 72.5 | 160 | 17 US-10-909-119-51 | Sequence 51, Appli |
| 12 | 98 | 69.0 | 28 | 14 US-10-060-102-3 | Sequence 3, Appli |
| 13 | 98 | 69.0 | 28 | 15 US-10-721-839-3 | Sequence 3, Appli |

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| 14 | 95 | 66.9 | 19 | 14 | US-10-060-102-21 | Sequence 21, Appli |
| 15 | 95 | 66.9 | 19 | 15 | US-10-721-839-21 | Sequence 21, Appli |
| 16 | 95 | 66.9 | 21 | 14 | US-10-060-102-23 | Sequence 23, Appli |
| 17 | 95 | 66.9 | 21 | 15 | US-10-721-839-23 | Sequence 23, Appli |
| 18 | 91 | 64.1 | 18 | 14 | US-10-060-102-22 | Sequence 22, Appli |
| 19 | 91 | 64.1 | 18 | 15 | US-10-721-839-22 | Sequence 22, Appli |
| 20 | 91 | 64.1 | 20 | 14 | US-10-060-102-24 | Sequence 24, Appli |
| 21 | 91 | 64.1 | 20 | 15 | US-10-721-839-24 | Sequence 24, Appli |
| 22 | 90 | 63.4 | 18 | 9 | US-09-840-009-2 | Sequence 2, Appli |
| 23 | 90 | 63.4 | 18 | 9 | US-09-840-009-9 | Sequence 9, Appli |
| 24 | 90 | 63.4 | 18 | 9 | US-09-840-009-16 | Sequence 16, Appli |
| 25 | 90 | 63.4 | 18 | 9 | US-09-840-009-23 | Sequence 23, Appli |
| 26 | 90 | 63.4 | 18 | 9 | US-09-840-009-30 | Sequence 30, Appli |
| 27 | 90 | 63.4 | 18 | 14 | US-10-060-102-9 | Sequence 9, Appli |
| 28 | 90 | 63.4 | 18 | 14 | US-10-060-102-12 | Sequence 12, Appli |
| 29 | 90 | 63.4 | 18 | 15 | US-10-721-839-12 | Sequence 12, Appli |
| 30 | 90 | 63.4 | 18 | 15 | US-10-060-102-10 | Sequence 10, Appli |
| 31 | 88 | 62.0 | 18 | 14 | US-10-060-102-10 | Sequence 10, Appli |
| 32 | 88 | 62.0 | 18 | 14 | US-10-721-839-11 | Sequence 11, Appli |
| 33 | 88 | 62.0 | 18 | 15 | US-10-721-839-11 | Sequence 11, Appli |
| 34 | 88 | 62.0 | 18 | 15 | US-10-721-839-11 | Sequence 11, Appli |
| 35 | 85 | 59.9 | 18 | 9 | US-09-840-009-4 | Sequence 4, Appli |
| 36 | 85 | 59.9 | 18 | 9 | US-09-840-009-8 | Sequence 8, Appli |
| 37 | 85 | 59.9 | 18 | 9 | US-09-840-009-11 | Sequence 11, Appli |
| 38 | 85 | 59.9 | 18 | 9 | US-09-840-009-15 | Sequence 15, Appli |
| 39 | 85 | 59.9 | 18 | 9 | US-09-840-009-18 | Sequence 18, Appli |
| 40 | 85 | 59.9 | 18 | 9 | US-09-840-009-22 | Sequence 22, Appli |
| 41 | 85 | 59.9 | 18 | 9 | US-09-840-009-25 | Sequence 25, Appli |
| 42 | 85 | 59.9 | 18 | 9 | US-09-840-009-29 | Sequence 29, Appli |
| 43 | 85 | 59.9 | 18 | 14 | US-10-060-102-25 | Sequence 25, Appli |
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| 45 | 84 | 59.2 | 18 | 9 | US-09-840-009-5 | Sequence 5, Appli |

ALIGNMENTS

RESULT 1
US-10-060-102-8
Sequence 8, Application US/10060102
Publication No. US20030022829A1
GENERAL INFORMATION:
APPLICANT: MAURY, WENDY
APPLICANT: STAPLETON, JACK
APPLICANT: ROLLER, RICHARD
APPLICANT: STINSKI, MARK
APPLICANT: MCCRAY, PAUL B.
TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMAL
FILE REFERENCE: IOWA:03US
CURRENT FILING DATE: 2002-02-22
PRIORITY FILING DATE: 2001-08-01
PRIORITY APPLICATION NUMBER: 60/303,368
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: 60/265,270
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 29
TYPE: PPT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-060-102-8

Query Match 100.0%; Score 142; DB 14; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.9e-13;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Query 1 KNLRRIRKIHIIKKYGPITLIRITIG 29

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 2, 2005, 12:18:40 ; Search time 27.5419 seconds
(without alignments)
78.601 Million cell updates/sec

Title: US-09-642-744D-28

Sequence: 1 KNLRRIRKRIHIKKYGPITLIRIRIG 29

Scoring tables: BLOSUM62

Searched: Gapop 10.0, Gapext 0.5

513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|------------------|
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| 2 | 90 | 63.4 | 18 | 4 | US-09-840-009-2 |
| 3 | 90 | 63.4 | 18 | 4 | US-09-840-009-9 |
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| 5 | 90 | 63.4 | 18 | 4 | US-09-840-009-23 |
| 6 | 90 | 63.4 | 18 | 4 | US-09-840-009-30 |
| 7 | 85 | 59.9 | 18 | 4 | US-09-840-009-4 |
| 8 | 85 | 59.9 | 18 | 4 | US-09-840-009-8 |
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| 10 | 85 | 59.9 | 18 | 4 | US-09-840-009-15 |
| 11 | 85 | 59.9 | 18 | 4 | US-09-840-009-18 |
| 12 | 85 | 59.9 | 18 | 4 | US-09-840-009-22 |
| 13 | 85 | 59.9 | 18 | 4 | US-09-840-009-25 |
| 14 | 85 | 59.9 | 18 | 4 | US-09-840-009-29 |
| 15 | 84 | 59.2 | 18 | 4 | US-09-840-009-5 |
| 16 | 84 | 59.2 | 18 | 4 | US-09-840-009-12 |
| 17 | 84 | 59.2 | 18 | 4 | US-09-840-009-19 |
| 18 | 84 | 59.2 | 18 | 4 | US-09-840-009-26 |
| 19 | 83 | 58.5 | 18 | 4 | US-09-840-009-6 |
| 20 | 83 | 58.5 | 18 | 4 | US-09-840-009-7 |
| 21 | 83 | 58.5 | 18 | 4 | US-09-840-009-13 |
| 22 | 83 | 58.5 | 18 | 4 | US-09-840-009-14 |
| 23 | 83 | 58.5 | 18 | 4 | US-09-840-009-20 |
| 24 | 83 | 58.5 | 18 | 4 | US-09-840-009-21 |
| 25 | 83 | 58.5 | 18 | 4 | US-09-840-009-27 |
| 26 | 83 | 58.5 | 18 | 4 | US-09-840-009-28 |
| 27 | 82 | 57.7 | 18 | 4 | US-09-840-009-3 |

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| 28 | 82 | 57.7 | 18 | 4 | US-09-840-009-10 | Sequence 10, Appl |
| 29 | 82 | 57.7 | 18 | 4 | US-09-840-009-17 | Sequence 17, Appl |
| 30 | 82 | 57.7 | 18 | 4 | US-09-840-009-24 | Sequence 24, Appl |
| 31 | 82 | 57.7 | 18 | 4 | US-09-840-009-31 | Sequence 31, Appl |
| 32 | 76 | 53.5 | 18 | 4 | US-09-840-009-34 | Sequence 34, Appl |
| 33 | 76 | 53.5 | 18 | 4 | US-09-840-009-35 | Sequence 35, Appl |
| 34 | 74 | 52.1 | 18 | 4 | US-09-840-009-32 | Sequence 32, Appl |
| 35 | 74 | 52.1 | 18 | 4 | US-09-840-009-33 | Sequence 33, Appl |
| 36 | 70 | 49.3 | 18 | 4 | US-09-840-009-1 | Sequence 1, Appl |
| 37 | 67 | 47.2 | 159 | 4 | US-09-917-340-34 | Sequence 14, Appl |
| 38 | 65 | 45.8 | 18 | 4 | US-09-840-009-36 | Sequence 36, Appl |
| 39 | 65 | 45.8 | 18 | 4 | US-09-840-009-37 | Sequence 37, Appl |
| 40 | 53.5 | 37.7 | 205 | 3 | US-09-134-001C-4766 | Sequence 4766, Ap |
| 41 | 52 | 36.6 | 42 | 4 | US-09-785-0598-7 | Sequence 7, Appl |
| 42 | 52 | 36.6 | 48 | 4 | US-09-785-0598-8 | Sequence 8, Appl |
| 43 | 51 | 35.9 | 167 | 4 | US-09-107-532A-7260 | Sequence 7260, Ap |
| 44 | 50 | 35.2 | 36 | 4 | US-09-785-0598-6 | Sequence 6, Appl |
| 45 | 50 | 35.2 | 169 | 4 | US-09-270-767-35406 | Sequence 35406, A |

ALIGNMENTS

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RESULT 1
US-09-917-340-36
Sequence 36, Application US/09917340
Patent No. 6696238
GENERAL INFORMATION:
APPLICANT: Murphy, Christopher J.
APPLICANT: McAnuley, Jonathan F.
APPLICANT: Reid, Ted W.
TITLE OF INVENTION: Transplant Media
FILE REFERENCE: TPLANT-06468
CURRENT APPLICATION NUMBER: US/09/917,340
PRIOR FILING DATE: 2001-07-29
PRIOR APPLICATION NUMBER: 60/221,632
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 60/249,602
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/290,932
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 96
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 36
LENGTH: 160
TYPE: PRT
ORGANISM: Ovis aries
US-09-917-340-36
Query Match 72.5%; Score 103; DB 4; Length 160;
Best Local Similarity 69.0%; Pred. No. 3.1e-07;
Matches 20; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
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DB 132 RGLRRGRKIAHGKYGPTVLRIRIRIG 160
RESULT 2
US-09-840-009-2
Sequence 2, Application US/09840009
Patent No. 6492328
GENERAL INFORMATION:
APPLICANT: Lehter, Robert I.
APPLICANT: Tack, Brian F.
TITLE OF INVENTION: NOUSPINS: ANTIMICROBIAL PEPTIDES
FILE REFERENCE: 06510-195WO
CURRENT APPLICATION NUMBER: US/09/840,009
CURRENT FILING DATE: 2001-04-19
PRIOR APPLICATION NUMBER: US 09/606,858
PRIOR FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 37
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Copyright (c) 1993 - 2005 CompuGen Ltd.

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Run on: May 2, 2005, 12:21:40 ; Search time 10.5419 Seconds

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155.160 Million cell updates/sec

Title: US-09-642-744D-26

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: p1r2: *
3: p1r3: *
4: p1r4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 2 | 56 | 69.1 | 173 | 2 S70521 | cathelin-related p |
| 3 | 49 | 60.5 | 168 | 1 F64494 | conserved hypochet |
| 4 | 48 | 59.3 | 117 | 1 H71166 | hypothetical prote |
| 5 | 48 | 59.3 | 117 | 2 E75065 | hypothetical prote |
| 6 | 48 | 59.3 | 324 | 2 T07982 | probable choline-p |
| 7 | 48 | 59.3 | 326 | 2 T07983 | choline-phosphate |
| 8 | 48 | 59.3 | 1156 | 2 B70356 | chromosome assembl |
| 9 | 46 | 56.8 | 392 | 2 B85363 | hypothetical prote |
| 10 | 46 | 56.8 | 430 | 2 D70221 | conserved hypochet |
| 11 | 45 | 55.6 | 167 | 2 S68967 | antibacterial pept |
| 12 | 45 | 55.6 | 329 | 2 T07981 | probable choline-p |
| 13 | 45 | 55.6 | 331 | 2 T07980 | DNA ligase (NAD de |
| 14 | 45 | 55.6 | 663 | 2 D97047 | hypothetical prote |
| 15 | 45 | 55.6 | 829 | 2 T32744 | ATP-dependent deox |
| 16 | 45 | 55.6 | 1166 | 2 A39432 | hypoxanthine-guan |
| 17 | 44 | 54.3 | 178 | 2 H97293 | hypothetical prote |
| 18 | 44 | 54.3 | 280 | 2 C64471 | integrinase/recomb |
| 19 | 44 | 54.3 | 387 | 2 F95130 | UDP-N-acetylglucos |
| 20 | 44 | 54.3 | 425 | 2 H70410 | glucose inhibited |
| 21 | 44 | 54.3 | 519 | 2 T51496 | hypothetical prote |
| 22 | 44 | 54.3 | 611 | 2 B90543 | hypothetical prote |
| 23 | 43 | 53.1 | 93 | 2 C81812 | hypothetical prote |
| 24 | 43 | 53.1 | 110 | 2 B64591 | hypothetical prote |
| 25 | 43 | 53.1 | 110 | 2 A71921 | hypothetical prote |
| 26 | 43 | 53.1 | 194 | 2 G64322 | conserved hypochet |
| 27 | 43 | 53.1 | 216 | 2 F69300 | beta-lactamase (EC |
| 28 | 43 | 53.1 | 281 | 1 PMSAP | hypothetical prote |
| 29 | 43 | 53.1 | 361 | 2 T25196 | hypothetical prote |

ALIGNMENTS

| | | | | | |
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| 30 | 43 | 53.1 | 428 | 2 C26532 | 5-enolpyruvylshik |
| 31 | 43 | 53.1 | 953 | 2 S54478 | probable membrane |
| 32 | 42 | 51.9 | 135 | 2 A29504 | hypothetical 16k p |
| 33 | 42 | 51.9 | 173 | 2 S55150 | hypothetical prote |
| 34 | 42 | 51.9 | 183 | 2 D84473 | En/Spm-like transp |
| 35 | 42 | 51.9 | 235 | 2 F70405 | hypothetical prote |
| 36 | 42 | 51.9 | 267 | 2 T07215 | ribosomal protein |
| 37 | 42 | 51.9 | 270 | 2 H64248 | hypothetical prote |
| 38 | 42 | 51.9 | 309 | 2 F84952 | homoserine kinase |
| 39 | 42 | 51.9 | 313 | 2 A70441 | glycerol-3-phospha |
| 40 | 42 | 51.9 | 332 | 2 H84730 | probable phospholi |
| 41 | 42 | 51.9 | 380 | 2 F70399 | hydrogenase expres |
| 42 | 42 | 51.9 | 428 | 1 D71155 | probable methyl-ac |
| 43 | 42 | 51.9 | 522 | 2 C96608 | hypothetical prote |
| 44 | 42 | 51.9 | 629 | 2 S20516 | dnak-type molecule |
| 45 | 42 | 51.9 | 712 | 2 AE2365 | dnak-type molecule |

RESULT 1
JQ1171
18K lipopolysaccharide-binding protein precursor - rabbit
N:Alternate names: 18K cationic protein
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 06-Dec-1996
R:Larrick, J.W.; Morgan, J.G.; Palings, I.; Hirata, M.; Yen, M.H.
Biochem. Biophys. Res. Commun. 179, 170-175, 1991
A:Title: Complementary DNA sequence of rabbit CAP18-a unique lipopolysaccharide binding
A:Reference number: JQ1171; MUID:91354246; PMID:1883348
A:Accession: JQ1171
A:Molecule type: mRNA
A:Residues: 1-171 <LAR>
A:Experimental source: bone marrow
A:Accession: PS0226
A:Molecule type: protein
A:Residues: 135-159, 'QIGQL' <LA2>
A:Note: 157-Asp was also found
C:Superfamily: cathelin; cystatin homology
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-171/Product: 18K lipopolysaccharide-binding protein #status predicted <MAT>

Query Match 100.0%; Score 81; DB 2; Length 171;
Best Local Similarity 100.0%; Pred. NO. 0.00016;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIKELKKIKGKIQGL 17
DB 146 KIKELKKIKGKIQGL 162

RESULT 2
S70521
cathelin-related protein precursor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
R:Poppeeva, A.E.; Zinovjeva, M.V.; Visser, J.W.M.; Zijlman, J.M.J.M.; Fibbe, W.E.; Bel
FEBS Lett. 391, 5-8, 1996
A:Title: A novel murine cathelin-like protein expressed in bone marrow.
A:Reference number: S70521; MUID:96326596; PMID:8706928
A:Accession: S70521
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-173 <POP>
A:Cross-references: UNIPROT:P51437; EMBL:X94353; NID:g1177533; PIDD:CA64078.1; PID:g11
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-144/Domain: propeptide #status predicted <PRO>
F:145-173/Product: cathelin-related protein #status predicted <MAT>

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 2, 2005, 13:03:56 ; Search time 46.2514 Seconds

(without alignments)
122.435 Million cell updates/sec

Title: US-09-642-744d-26

Sequence: 1 KIKKKLKKIKGKIGGL 17

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1426032 seqs, 333106140 residues

Total number of hits satisfying chosen parameters: 1426032

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Database : Published Applications AA:

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2: /cgn2_6/ptodata/1/pubppa/PCT_NEW_PUB.pap:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 2 | 81 | 100.0 | 37 | 14 US-10-060-102-5 | Sequence 5, Appl1 |
| 3 | 81 | 100.0 | 37 | 15 US-10-721-839-5 | Sequence 5, Appl1 |
| 4 | 74 | 91.4 | 37 | 16 US-10-344-709C-15 | Sequence 15, Appl1 |
| 5 | 74 | 91.4 | 171 | 16 US-10-344-709C-7 | Sequence 2, Appl1 |
| 6 | 56 | 69.1 | 31 | 17 US-10-399-442A-2 | Sequence 1, Appl1 |
| 7 | 56 | 69.1 | 32 | 16 US-10-344-709C-1 | Sequence 599, App |
| 8 | 56 | 69.1 | 36 | 17 US-10-470-048B-599 | Sequence 1, Appl1 |
| 9 | 56 | 69.1 | 39 | 15 US-10-060-103-1 | Sequence 1, Appl1 |
| 10 | 56 | 69.1 | 39 | 15 US-10-721-839-1 | Sequence 1, Appl1 |
| 11 | 56 | 69.1 | 173 | 16 US-10-344-709C-5 | Sequence 5, Appl1 |
| 12 | 50 | 61.7 | 36 | 14 US-10-269-171A-2 | Sequence 2, Appl1 |
| 13 | 49 | 60.5 | 39 | 14 US-10-060-102-2 | Sequence 2, Appl1 |

| | | | | | | |
|----|------|------|------|----|----------------------|-------------------|
| 14 | 49 | 60.5 | 39 | 15 | US-10-721-839-2 | Sequence 2, Appl1 |
| 15 | 48 | 59.3 | 324 | 15 | US-10-389-566-1171 | Sequence 1171, Ap |
| 16 | 48 | 59.3 | 326 | 14 | US-10-233-926-25 | Sequence 25, Appl |
| 17 | 48 | 59.3 | 326 | 15 | US-10-389-566-1172 | Sequence 1172, Ap |
| 18 | 46 | 56.8 | 1156 | 15 | US-10-369-493-43 | Sequence 43, Appl |
| 19 | 46 | 56.8 | 104 | 15 | US-10-424-599-245241 | Sequence 245241, |
| 20 | 46 | 56.8 | 190 | 15 | US-10-424-599-225312 | Sequence 225312, |
| 21 | 46 | 56.8 | 194 | 14 | US-10-389-566-673 | Sequence 6, Appl1 |
| 22 | 46 | 56.8 | 318 | 15 | US-10-389-566-673 | Sequence 673, App |
| 23 | 46 | 56.8 | 318 | 15 | US-10-389-566-674 | Sequence 674, App |
| 24 | 46 | 56.8 | 363 | 14 | US-10-233-926-20 | Sequence 20, Appl |
| 25 | 45 | 55.6 | 37 | 16 | US-10-344-709C-12 | Sequence 12, Appl |
| 26 | 45 | 55.6 | 157 | 16 | US-10-767-701-47315 | Sequence 47315, A |
| 27 | 45 | 55.6 | 275 | 16 | US-10-437-963-1174 | Sequence 1174, Ap |
| 28 | 45 | 55.6 | 329 | 15 | US-10-389-566-1173 | Sequence 1173, Ap |
| 29 | 45 | 55.6 | 331 | 14 | US-10-233-926-23 | Sequence 23, Appl |
| 30 | 45 | 55.6 | 331 | 15 | US-10-389-566-1173 | Sequence 1174, Ap |
| 31 | 45 | 55.6 | 331 | 15 | US-10-389-566-1174 | Sequence 51673, A |
| 32 | 45 | 55.6 | 663 | 15 | US-10-282-122A-51673 | Sequence 5082, Ap |
| 33 | 45 | 55.6 | 829 | 15 | US-10-369-493-5082 | Sequence 148381, |
| 34 | 44 | 54.3 | 60 | 16 | US-10-437-963-148381 | Sequence 40325, A |
| 35 | 44 | 54.3 | 199 | 15 | US-10-425-114-40325 | Sequence 194227, |
| 36 | 44 | 54.3 | 216 | 15 | US-10-424-599-194227 | Sequence 2252, Ap |
| 37 | 44 | 54.3 | 387 | 17 | US-10-472-928-2252 | Sequence 184421, |
| 38 | 44 | 54.3 | 477 | 16 | US-10-437-963-184421 | Sequence 112025, |
| 39 | 44 | 54.3 | 692 | 16 | US-10-437-963-112025 | Sequence 53473, A |
| 40 | 43.5 | 53.7 | 72 | 16 | US-10-282-122A-53473 | Sequence 56766, A |
| 41 | 43 | 53.1 | 118 | 15 | US-10-767-701-56766 | Sequence 225574, |
| 42 | 43 | 53.1 | 79 | 15 | US-10-424-599-225574 | Sequence 8, Appl1 |
| 43 | 43 | 53.1 | 168 | 16 | US-09-882-227-8 | Sequence 59241, A |
| 44 | 43 | 53.1 | 168 | 16 | US-10-767-701-59241 | Sequence 230427, |
| 45 | 43 | 53.1 | 274 | 15 | US-10-424-599-230427 | |

ALIGNMENTS

RESULT 1
US-10-131-433-1
Sequence 1, Application US/10131433
Publication No. US20030054422A1
GENERAL INFORMATION:
APPLICANT: UNILEVER, PLC
TITLE OF INVENTION: Lipopolyasaccharide Immunoassay and Test Device
FILE REFERENCE: Lipopolyasaccharide Immunoassay
CURRENT FILING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: US/10/131,433
PRIORITY FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 32
TYPE: PRT
ORGANISM: Lactine
US-10-131-433-1

Query Match 100.0% Score 81; DB 14; Length 32;
Best Local Similarity 100.0% Pred No. 9.1e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIKKKLKKIKGKIGGL 17
DB 12 KIKKKLKKIKGKIGGL 28

RESULT 2
US-10-060-102-5
Sequence 5, Application US/10060102
Publication No. US2003002829A1
GENERAL INFORMATION:
APPLICANT: MAURY, WENDY
STAPLETON, JACK

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:18:40 ; Search time 16.1453 Seconds

(Without alignments)
78.601 Million cell updates/sec

Title: US-09-642-744D-26

Sequence: 1 KIKKXKKIKGKIGGL 17

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 1 | 81 | 100.0 | 171 | US-08-313-681A-4 | Sequence 4, Appl |
| 2 | 81 | 100.0 | 171 | US-09-322-911-4 | Sequence 4, Appl |
| 3 | 81 | 100.0 | 171 | US-08-313-681A-7 | Sequence 7, Appl |
| 4 | 63 | 77.8 | 29 | US-09-332-911-7 | Sequence 7, Appl |
| 5 | 63 | 77.8 | 29 | PCT-US95-12080-4 | Sequence 25, Appl |
| 6 | 59.3 | 69.1 | 33 | US-09-735-846-25 | Sequence 25, Appl |
| 7 | 48 | 59.3 | 32 | US-09-134-001C-4678 | Sequence 6, Appl |
| 8 | 47 | 58.0 | 30 | US-09-735-846-6 | Sequence 24, Appl |
| 9 | 46 | 56.8 | 363 | US-09-735-846-20 | Sequence 24, Appl |
| 10 | 45 | 55.6 | 329 | US-09-735-846-24 | Sequence 24, Appl |
| 11 | 45 | 55.6 | 331 | US-09-735-846-23 | Sequence 24, Appl |
| 12 | 44 | 54.3 | 90 | US-09-489-039A-11599 | Sequence 8456, Ap |
| 13 | 44 | 54.3 | 434 | US-09-489-039A-8456 | Sequence 8456, Ap |
| 14 | 43 | 53.1 | 281 | US-08-284-465-6 | Sequence 42, Appl |
| 15 | 43 | 53.1 | 428 | US-08-476-008-42 | Sequence 42, Appl |
| 16 | 43 | 53.1 | 428 | US-08-306-063-42 | Sequence 42, Appl |
| 17 | 43 | 53.1 | 428 | US-09-137-440-42 | Sequence 42, Appl |
| 18 | 43 | 53.1 | 428 | US-09-137-440-42 | Sequence 42, Appl |
| 19 | 43 | 53.1 | 1105 | US-09-540-236-3299 | Sequence 3299, Ap |
| 20 | 42 | 51.9 | 952 | US-09-328-352-5611 | Sequence 5611, Ap |
| 21 | 41.5 | 51.2 | 1770 | US-10-144-198-44 | Sequence 44, Appl |
| 22 | 41.5 | 51.2 | 2221 | US-10-144-198-44 | Sequence 44, Appl |
| 23 | 41 | 50.6 | 99 | US-09-134-001C-3848 | Sequence 3848, Ap |
| 24 | 41 | 50.6 | 101 | US-09-461-697-204 | Sequence 204, App |
| 25 | 41 | 50.6 | 161 | US-09-640-211A-1054 | Sequence 1054, Ap |
| 26 | 41 | 50.6 | 390 | US-09-543-681A-5753 | Sequence 5753, Ap |
| 27 | 41 | 50.6 | 450 | US-09-248-796A-15183 | Sequence 15183, A |

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| 28 | 41 | 50.6 | 519 | US-08-397-445D-2 | Sequence 2, Appl |
| 29 | 41 | 50.6 | 617 | US-09-134-001C-4012 | Sequence 4012, Ap |
| 30 | 41 | 50.6 | 2710 | US-08-568-459A-12 | Sequence 12, Appl |
| 31 | 41 | 50.6 | 2710 | US-08-487-826B-12 | Sequence 12, Appl |
| 32 | 41 | 50.6 | 2710 | US-09-210-288-12 | Sequence 12, Appl |
| 33 | 41 | 50.6 | 3060 | US-08-487-826B-14 | Sequence 14, Appl |
| 34 | 41 | 50.6 | 3421 | US-09-452-638-53 | Sequence 53, Appl |
| 35 | 40.5 | 50.0 | 319 | US-09-328-352-6042 | Sequence 6042, Ap |
| 36 | 40 | 49.4 | 23 | US-08-505-486-60 | Sequence 60, Appl |
| 37 | 40 | 49.4 | 23 | US-08-801-028-60 | Sequence 60, Appl |
| 38 | 40 | 49.4 | 23 | US-09-340-154-60 | Sequence 60, Appl |
| 39 | 40 | 49.4 | 23 | US-09-482-611B-60 | Sequence 60, Appl |
| 40 | 40 | 49.4 | 23 | PCT-US95-09338-60 | Sequence 60, Appl |
| 41 | 40 | 49.4 | 23 | PCT-US95-09338-60 | Sequence 60, Appl |
| 42 | 40 | 49.4 | 27 | US-08-505-486-61 | Sequence 61, Appl |
| 43 | 40 | 49.4 | 27 | US-08-505-486-62 | Sequence 62, Appl |
| 44 | 40 | 49.4 | 27 | US-08-801-028-61 | Sequence 61, Appl |
| 45 | 40 | 49.4 | 27 | US-08-801-028-62 | Sequence 62, Appl |

ALIGNMENTS

RESULT 1
US-08-313-681A-4
Sequence 4, Application US/08313681A
Patent No. 5618675
GENERAL INFORMATION:
APPLICANT: Larrick, James W.
APPLICANT: Wright, Susan C.
APPLICANT: Hirata, Mishimasa
TITLE OF INVENTION: Human Cationic Proteins Having
TITLE OF INVENTION: Lipopolysaccharide Binding and Anti-Coagulant Activity
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,681A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15325-9-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 171 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-313-681A-4
Query Match 100.0% Score 81; DB 1; Length 171;
Best Local Similarity 100.0%; Pred No. 0.00038;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KIKKXKKIKGKIGGL 17
DB 146 KIKKXKKIKGKIGGL 162

AA870648 to AA870665 represent antimicrobial peptides (1), of which
AA870648, AA870664, AA870674 and AA870675 are derived from the ovine
SNAP 29 cathelicidin family peptide, and AA870665 to AA870673 are derived
from the human RCP18 cathelicidin family peptide. (1) have antibiologic,
CC antimicrobial and antiviral activities, and can be used as microbial
CC growth and proliferation inhibitors, and in gene therapy. (1) are useful
CC for inhibiting microbial growth in an environment capable of sustaining
CC such growth, for inhibiting microbial growth or strain in a host, and
CC inhibiting the growth of drug-resistant microbial strains such as
CC *Pseudomonas aeruginosa*, *Burkholderia cepacia*, *Alcaligenes* and *Xanthomonas*
CC

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Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 2, 2005, 12:17:06 ; Search time 46.8017 seconds
(without alignments) 164.122 Million cell updates/sec

Title: US-09-642-744D-25

Perfect score: 73

Sequence: 1 KIKKKKKIKGKIQG 15

Scoring table:

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Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 2 | 56 | 76.7 | 173 | 1 CRAM_MOUSE | P51437 mus musculi |
| 3 | 51 | 69.9 | 366 | 2 O8VQ90 | O8VQ90 uncultured |
| 4 | 50 | 68.5 | 1123 | 2 O6S255 | O6S255 streptococc |
| 5 | 49 | 67.1 | 170 | 2 O9GLV5 | O9GLV5 macaca mula |
| 6 | 49 | 67.1 | 171 | 2 O7IKM5 | O7IKM5 ratcus norv |
| 7 | 48 | 65.8 | 123 | 2 O9NHL6 | O9NHL6 plasmodium |
| 8 | 48 | 65.8 | 270 | 2 O6ETR2 | O6ETR2 candida gla |
| 9 | 48 | 65.8 | 324 | 2 O42621 | O42621 brassica na |
| 10 | 48 | 65.8 | 326 | 2 O42622 | O42622 brassica na |
| 11 | 47 | 64.4 | 68 | 2 O970H2 | O970H2 sulfobolus |
| 12 | 47 | 64.4 | 170 | 1 Y959_METIA | Y959_METIA |
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| 14 | 47 | 64.4 | 179 | 2 O6UIV7 | O6UIV7 staphylococ |
| 15 | 47 | 64.4 | 224 | 2 O9S0D9 | O9S0D9 staphylococ |
| 16 | 47 | 64.4 | 244 | 2 O87584 | O87584 borrelia bu |
| 17 | 47 | 64.4 | 281 | 2 O8CMM3 | O8CMM3 staphylococ |
| 18 | 47 | 64.4 | 366 | 2 O8VQ88 | O8VQ88 uncultured |
| 19 | 46 | 63.0 | 117 | 1 PFDB_PYPAB | PFDB_PYPAB |
| 20 | 46 | 63.0 | 284 | 1 PFDB_PYPFU | PFDB_PYPFU |
| 21 | 46 | 63.0 | 392 | 2 O65549 | O65549 arabidopsis |
| 22 | 46 | 63.0 | 405 | 2 O8VYD9 | O8VYD9 arabidopsis |
| 23 | 46 | 63.0 | 889 | 2 O8XMY3 | O8XMY3 clostridium |
| 24 | 46 | 63.0 | 1156 | 2 O66878 | O66878 alexa aeo |
| 25 | 45 | 61.6 | 117 | 1 PFDB_PYPAB | PFDB_PYPAB |
| 26 | 45 | 61.6 | 117 | 1 PFDB_PYPAB | PFDB_PYPAB |
| 27 | 45 | 61.6 | 130 | 2 O6S8U8 | O6S8U8 plasmodium |
| 28 | 45 | 61.6 | 130 | 2 O8J6C9 | O8J6C9 human immun |
| 29 | 45 | 61.6 | 172 | 2 O6TJ20 | O6TJ20 canis fami |
| 30 | 45 | 61.6 | 183 | 2 O7VCL9 | O7VCL9 prochloroco |
| 31 | 45 | 61.6 | 329 | 2 O42620 | O42620 brassica na |

ALIGNMENTS

| RESULT 1 | CP18_RABIT | STANDARD; | PRT; | 171 AA. |
|----------|--|-----------|------|---------|
| ID | CP18_RABIT | | | |
| AC | P25230; | | | |
| DT | 01-MAY-1992 (Rel. 22, Created) | | | |
| DT | 01-MAY-1992 (Rel. 22, Last sequence update) | | | |
| DT | 25-OCT-2004 (Rel. 45, Last annotation update) | | | |
| DE | Antimicrobial protein CAP18 precursor (18 kDa lipopolysaccharide-binding protein) (18 kDa cationic protein) (CAP18-A). | | | |
| GN | Name=CAP18; | | | |
| OS | Oryctolagus cuniculus (Rabbit). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus. | | | |
| OX | NCBI_TaxID=9986; | | | |
| RN | (1) | | | |
| RP | SEQUENCE FROM N.A., AND SEQUENCE OF 135-159. | | | |
| RC | TISSUE=Bone marrow; | | | |
| RX | MEDLINE=91354246; PubMed=1883348; | | | |
| RA | Larrick J.W., Morgan J.G., Palings I., Hirata M., Yen M.H.; | | | |
| RT | "Complementary DNA sequence of rabbit CAP18 -- a unique | | | |
| RL | lipopolysaccharide binding protein."; | | | |
| RN | Biochem. Biophys. Res. Commun. 179:170-175(1991). | | | |
| RP | (2) | | | |
| RX | SEQUENCE OF 135-159, AND CHARACTERIZATION. | | | |
| RA | MEDLINE=94178952; PubMed=8132348; | | | |
| RT | Hirata M., Shimomura Y., Yoshida M., Morgan J.G., Palings I., | | | |
| RL | Wilson D., Yen M.H., Wright S.C., Larrick J.W.; | | | |
| RT | "Characterization of a rabbit cationic protein (CAP18) with | | | |
| RL | lipopolysaccharide-inhibitory activity."; | | | |
| RN | Infect. Immun. 62:1421-1426(1994). | | | |
| RP | (3) | | | |
| RX | SEQUENCE OF 135-154, AND CHARACTERIZATION. | | | |
| RA | MEDLINE=94075827; PubMed=8254193; | | | |
| RT | Larrick J.W., Hirata M., Zheng H., Zhong J., Bolin D., | | | |
| RL | Cavallion J.-M., Warren H.S., Wright S.C.; | | | |
| RT | "A novel granulocyte-derived peptide with lipopolysaccharide- | | | |
| RL | neutralizing activity."; | | | |
| RN | J. Immunol. 152:231-240(1994). | | | |
| RP | (4) | | | |
| RX | CHARACTERIZATION. | | | |
| RA | MEDLINE=9418064; PubMed=8313956; DOI=10.1016/0014-5793(94)80395-1; | | | |
| RT | Tossi A., Scocchi M., Skerlavaj B., Gennaro R.; | | | |
| RL | "Identification and characterization of a primary antibacterial domain | | | |
| RT | in CAP18, a lipopolysaccharide binding protein from rabbit | | | |
| RL | leukocytes."; | | | |
| RN | FEBS Lett. 339:108-112(1994). | | | |
| RP | (5) | | | |
| RX | STRUCTURE BY NMR OF 135-166. | | | |
| RA | MEDLINE=95377455; PubMed=7649303; DOI=10.1016/0014-5793(95)00792-8; | | | |
| RT | Chen C., Brock R., Luh F., Chou P.-J., Larrick J.W., Huang R.-F., | | | |
| RL | Huang T.-H.; | | | |
| RT | "The solution structure of the active domain of CAP18 -- a | | | |
| RL | lipopolysaccharide binding protein from rabbit leukocytes."; | | | |
| | FEBS Lett. 370:46-52(1995). | | | |

| | | | | | | |
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| 32 | 45 | 61.6 | 331 | 2 | O42619 | O42619 brassica na |
| 33 | 45 | 61.6 | 352 | 2 | O74ML2 | O74ML2 nanoarchaeu |
| 34 | 45 | 61.6 | 473 | 2 | O9M8K5 | O9M8K5 arabidopsis |
| 35 | 45 | 61.6 | 526 | 2 | O649R7 | O649R7 uncultured |
| 36 | 45 | 61.6 | 569 | 2 | O9Z8R6 | O9Z8R6 zea mays (m |
| 37 | 45 | 61.6 | 663 | 2 | O970S8 | O970S8 clostridium |
| 38 | 45 | 61.6 | 665 | 2 | O8X162 | O8X162 clostridium |
| 39 | 45 | 61.6 | 668 | 2 | O89110 | O89110 clostridium |
| 40 | 45 | 61.6 | 3787 | 2 | O81126 | O81126 plasmodium |
| 41 | 44 | 60.3 | 56 | 2 | O6MM87 | O6MM87 bdellovibri |
| 42 | 44 | 60.3 | 150 | 2 | O8LL71 | O8LL71 theobroma c |
| 43 | 44 | 60.3 | 178 | 2 | O97EB1 | O97EB1 clostridium |
| 44 | 44 | 60.3 | 191 | 2 | O44867 | O44867 borrelia bu |
| 45 | 44 | 60.3 | 227 | 2 | O45026 | O45026 borrelia bu |

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:21:40 ; Search time 9.30168 Seconds

(without alignments)
155.160 Million cell updates/sec

Title: US-09-642-744d-25

Sequence: 1 KIKKLLKIKGKIQG 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: PIR 79:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|----------------------|
| 1 | 73 | 100.0 | 171 | 2 J01171 | 18K lipopolysaccha |
| 2 | 56 | 76.7 | 173 | 2 S70521 | cathelin-related p |
| 3 | 48 | 65.8 | 324 | 2 T07982 | probable choline-p |
| 4 | 48 | 65.8 | 326 | 2 T07983 | choline-phosphate |
| 5 | 47 | 64.4 | 188 | 1 F64494 | conserved hypochet |
| 6 | 46 | 63.0 | 392 | 2 B85363 | hypothetical prote |
| 7 | 45 | 63.0 | 1156 | 2 B70356 | chromosome assemb |
| 8 | 45 | 61.6 | 117 | 1 H71166 | hypothetical prote |
| 9 | 45 | 61.6 | 117 | 2 H75065 | hypothetical prote |
| 10 | 45 | 61.6 | 329 | 2 T07981 | probable choline-p |
| 11 | 45 | 61.6 | 331 | 2 T07980 | DNA ligase (NAD de |
| 12 | 45 | 61.6 | 663 | 2 D97047 | hypoxanthine-guan |
| 13 | 44 | 60.3 | 178 | 2 H97293 | hypothetical prote |
| 14 | 44 | 60.3 | 280 | 2 C64471 | integrinase/recombin |
| 15 | 44 | 60.3 | 425 | 2 F95130 | UDP-N-acetylglucos |
| 16 | 44 | 60.3 | 430 | 2 H70410 | conserved hypochet |
| 17 | 44 | 60.3 | 519 | 2 D70221 | hypothetical prote |
| 18 | 44 | 60.3 | 829 | 2 T51486 | hypothetical prote |
| 19 | 44 | 60.3 | 829 | 2 T32744 | hypothetical prote |
| 20 | 43 | 58.9 | 93 | 2 C81812 | hypothetical prote |
| 21 | 43 | 58.9 | 194 | 2 G64322 | hypothetical prote |
| 22 | 43 | 58.9 | 281 | 1 PMSAP | beta-lactamase (BC |
| 23 | 43 | 58.9 | 361 | 2 T25196 | hypothetical prote |
| 24 | 43 | 58.9 | 428 | 2 C26532 | 5-enolpyruvylshik |
| 25 | 42 | 57.5 | 167 | 2 S68957 | antibacterial pept |
| 26 | 42 | 57.5 | 173 | 2 S55150 | hypothetical prote |
| 27 | 42 | 57.5 | 267 | 2 T07215 | ribosomal protein |
| 28 | 42 | 57.5 | 332 | 2 H84730 | probable phosphol |
| 29 | 42 | 57.5 | 380 | 2 F70399 | hydrogenase expres |

| | | | | | |
|----|------|------|------|----------|---------------------|
| 30 | 42 | 57.5 | 611 | 2 E90543 | glucose inhibited |
| 31 | 42 | 57.5 | 629 | 2 S20516 | dnak-type molecule |
| 32 | 42 | 57.5 | 1558 | 2 B71603 | RESA-H3 antigen PR |
| 33 | 41 | 56.2 | 138 | 2 B90125 | 40S ribosomal prot |
| 34 | 41 | 56.2 | 148 | 2 A75041 | probable glycetol- |
| 35 | 41 | 56.2 | 274 | 2 C69444 | conserved hypochet |
| 36 | 41 | 56.2 | 313 | 2 A70441 | glycerol-3-phosphat |
| 37 | 41 | 56.2 | 369 | 2 F82333 | iron-sulfur cluste |
| 38 | 41 | 56.2 | 515 | 2 F96700 | protein F12A21.9 l |
| 39 | 41 | 56.2 | 517 | 2 D86804 | sensor protein kin |
| 40 | 41 | 56.2 | 558 | 2 E81037 | formate-tetrahydro |
| 41 | 41 | 56.2 | 558 | 2 E81037 | Probable formate-t |
| 42 | 41 | 56.2 | 712 | 2 AE2365 | dnak-type molecule |
| 43 | 41 | 56.2 | 729 | 2 T15076 | hypothetical prote |
| 44 | 41 | 56.2 | 865 | 2 D72206 | valine-tRNA ligase |
| 45 | 40.5 | 55.5 | 1019 | 2 F70342 | cation efflux syst |

ALIGNMENTS

RESULT 1

J01171 18K lipopolysaccharide-binding protein precursor - rabbit

N/Alternate names: 18K cationic protein

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 06-Dec-1996

C/Accession: J01171; PS0226

R/Larrick, J.W.; Morgan, J.G.; Pailings, I.; Hirata, M.; Yen, M.H.

Biochem. Biophys. Res. Commun. 179, 170-175, 1991

A/Title: Complementary DNA sequence of rabbit CAP18-a unique lipopolysaccharide binding

A/Reference number: J01171; MUID:91354246; PMID:1883348

A/Accession: J01171

A/Molecule type: mRNA

A/Residues: 1-171 <LAR>

A/Experimental source: bone marrow

A/Accession: PS0226

A/Molecule type: protein

A/Residues: 135-159, 'QITQQL' <LA2>

A/Note: 157-Aep was also found

C/Superfamily: cathelin; cystatin homology

F:1-29/Domain: signal sequence #status predicted <SIG>

F:30-171/Product: 18K lipopolysaccharide-binding protein #status predicted <MAT>

Query Match 100.0%; Score 73; DB 2; Length 171;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIKKLLKIKGKIQG 15

Db 146 KIKKLLKIKGKIQG 160

RESULT 2

S70521 cathelin-related protein precursor - mouse

C/Species: Mus musculus (house mouse)

C/Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004

C/Accession: S70521

R/Popovnev, A.E.; Zinovjeva, M.V.; Visser, J.W.M.; Zijlman, J.M.J.M.; Fabb, W.E.; Be

FEBS Lett. 391, 5-8, 1996

A/Title: A novel murine cathelin-like protein expressed in bone marrow.

A/Reference number: S70521; MUID:96326596; PMID:8706928

A/Accession: S70521

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-173 <POP>

A/Cross-references: UNIPROT:P51437; EMBL:X94353; NID:g1177533; PIDN:CAA64076.1; PID:g1

C/Superfamily: cathelin; cystatin homology

F:1-23/Domain: signal sequence #status predicted <SIG>

F:24-144/Domain: propeptide #status predicted <PRO>

F:145-173/Product: cathelin-related protein #status predicted <MAT>

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:18:40 ; Search time 14.2458 Seconds

(Without alignments)
78.601 Million cell updates/sec

Title: US-09-642-744D-25

Sequence: 1 KIRKJLKKIGQKIG 15

Scoring table:

BLOSUM62

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

1: /cgn2_6/prodata/1/iaa/5A COMB.pep.*
2: /cgn2_6/prodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/prodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/prodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/prodata/1/iaa/PCTUS COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|----------------------|
| 1 | 73 | 100.0 | 171 | 1 | US-08-313-681A-4 |
| 2 | 73 | 100.0 | 171 | 3 | US-09-322-911-4 |
| 3 | 61 | 83.6 | 29 | 1 | US-08-313-681A-7 |
| 4 | 61 | 83.6 | 29 | 3 | US-09-322-911-7 |
| 5 | 56 | 76.7 | 33 | 5 | PCT-US95-12080-4 |
| 6 | 48 | 65.8 | 326 | 4 | US-09-735-846-25 |
| 7 | 47 | 64.4 | 306 | 3 | US-09-134-001C-4678 |
| 8 | 46 | 63.0 | 194 | 4 | US-09-735-846-6 |
| 9 | 46 | 63.0 | 363 | 4 | US-09-735-846-20 |
| 10 | 45 | 61.6 | 329 | 4 | US-09-735-846-24 |
| 11 | 45 | 61.6 | 331 | 4 | US-09-735-846-23 |
| 12 | 44 | 60.3 | 434 | 4 | US-09-489-039A-8456 |
| 13 | 44 | 58.9 | 281 | 2 | US-08-284-465-6 |
| 14 | 43 | 58.9 | 428 | 1 | US-08-306-063-42 |
| 15 | 43 | 58.9 | 428 | 1 | US-08-306-063-42 |
| 16 | 43 | 58.9 | 428 | 1 | US-08-306-063-42 |
| 17 | 43 | 58.9 | 428 | 1 | US-08-306-063-42 |
| 18 | 43 | 58.9 | 428 | 1 | US-08-306-063-42 |
| 19 | 42 | 57.5 | 1105 | 4 | US-09-540-236-3299 |
| 20 | 41 | 56.2 | 90 | 4 | US-09-328-352-5611 |
| 21 | 41 | 56.2 | 390 | 4 | US-09-489-039A-11599 |
| 22 | 40.5 | 55.5 | 1770 | 4 | US-09-543-681A-5753 |
| 23 | 40.5 | 55.5 | 2221 | 4 | US-10-144-198-44 |
| 24 | 40 | 54.8 | 23 | 2 | US-08-505-486-60 |
| 25 | 40 | 54.8 | 23 | 3 | US-08-801-028-60 |
| 26 | 40 | 54.8 | 23 | 3 | US-09-340-154-60 |
| 27 | 40 | 54.8 | 23 | 4 | US-09-482-611B-60 |

| | | | | | | |
|----|----|------|-----|---|--------------------|-------------------|
| 28 | 40 | 54.8 | 23 | 5 | PCT-US95-09338-60 | Sequence 60, Appl |
| 29 | 40 | 54.8 | 23 | 5 | PCT-US95-09339-60 | Sequence 60, Appl |
| 30 | 40 | 54.8 | 27 | 2 | US-08-505-486-61 | Sequence 62, Appl |
| 31 | 40 | 54.8 | 27 | 2 | US-08-505-486-62 | Sequence 62, Appl |
| 32 | 40 | 54.8 | 27 | 3 | US-08-801-028-62 | Sequence 62, Appl |
| 33 | 40 | 54.8 | 27 | 3 | US-08-801-028-62 | Sequence 62, Appl |
| 34 | 40 | 54.8 | 27 | 3 | US-09-340-154-61 | Sequence 62, Appl |
| 35 | 40 | 54.8 | 27 | 3 | US-09-340-154-62 | Sequence 62, Appl |
| 36 | 40 | 54.8 | 27 | 4 | US-09-482-611B-61 | Sequence 62, Appl |
| 37 | 40 | 54.8 | 27 | 4 | US-09-482-611B-62 | Sequence 62, Appl |
| 38 | 40 | 54.8 | 27 | 5 | PCT-US95-09338-61 | Sequence 62, Appl |
| 39 | 40 | 54.8 | 27 | 5 | PCT-US95-09338-62 | Sequence 62, Appl |
| 40 | 40 | 54.8 | 27 | 5 | PCT-US95-09339-61 | Sequence 62, Appl |
| 41 | 40 | 54.8 | 27 | 5 | PCT-US95-09339-62 | Sequence 62, Appl |
| 42 | 40 | 54.8 | 28 | 1 | US-08-182-175A-4 | Sequence 62, Appl |
| 43 | 40 | 54.8 | 28 | 5 | PCT-US92-06412-4 | Sequence 4, Appl1 |
| 44 | 40 | 54.8 | 150 | 4 | US-09-732-210-1354 | Sequence 1354, Ap |
| 45 | 40 | 54.8 | 150 | 4 | US-09-732-210-1361 | Sequence 1361, Ap |

ALIGNMENTS

RESULT 1
US-08-313-681A-4
Sequence 4, Application US/08313681A
Patent No. 5618675

GENERAL INFORMATION:

APPLICANT: Larrick, James W.

APPLICANT: Wright, Susan C.

APPLICANT: Hirata, Mitsuhiro

TITLE OF INVENTION: Human Cationic Proteins Having

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Kourie and Crew

STREET: One Market Plaza, Steuart Tower, Suite 2000

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/313, 681A

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Heslin, James M.

REGISTRATION NUMBER: 29,541

REFERENCE/DOCKET NUMBER: 15325-9-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-326-2400

TELEFAX: 415-326-2422

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 171 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-313-681A-4

Query Match 100.0%; Score 73; DB 1; Length 171;

Best Local Similarity 100.0%; Pred. No. 0.003;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIRKJLKKIGQKIG 15
DB 146 KIRKJLKKIGQKIG 160

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 2, 2005, 12:17:06 ; Search time 46.8017 Seconds
(without alignments) 164.122 Million cell updates/sec

Title: US-09-642-744d-24

Perfect score: 75

Sequence: 1 RKFRNKIKKKIG 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 75 | 100.0 | 171 | 1 | CP18 RABIT |
| 2 | 48 | 64.0 | 361 | 1 | P25230 oryctolagus |
| 3 | 48 | 64.0 | 439 | 2 | Q978N0 |
| 4 | 48 | 64.0 | 497 | 2 | Q53589 |
| 5 | 48 | 64.0 | 497 | 2 | O8NT03 |
| 6 | 48 | 64.0 | 497 | 2 | O99R73 |
| 7 | 48 | 64.0 | 497 | 2 | O7A3D9 |
| 8 | 48 | 64.0 | 497 | 2 | Q6G6B0 |
| 9 | 47 | 62.7 | 1321 | 2 | O81BV4 |
| 10 | 46 | 61.3 | 169 | 1 | DEP1_VIBCH |
| 11 | 46 | 61.3 | 173 | 1 | GRAM_MOUSE |
| 12 | 46 | 61.3 | 321 | 2 | O7RAY0 |
| 13 | 46 | 61.3 | 400 | 2 | O89295 |
| 14 | 46 | 61.3 | 400 | 2 | O89297 |
| 15 | 46 | 61.3 | 400 | 2 | O89299 |
| 16 | 46 | 61.3 | 400 | 2 | O89304 |
| 17 | 46 | 61.3 | 400 | 2 | O89311 |
| 18 | 46 | 61.3 | 400 | 2 | O89315 |
| 19 | 46 | 61.3 | 400 | 2 | O89317 |
| 20 | 46 | 61.3 | 598 | 2 | O48537 |
| 21 | 46 | 61.3 | 778 | 2 | P89915 |
| 22 | 46 | 61.3 | 778 | 2 | O77X62 |
| 23 | 46 | 61.3 | 778 | 2 | O77X64 |
| 24 | 46 | 61.3 | 778 | 2 | O77X66 |
| 25 | 46 | 61.3 | 1111 | 1 | Y0EP_HAEIN |
| 26 | 46 | 61.3 | 1163 | 1 | POLG_YEPV8 |
| 27 | 46 | 61.3 | 1280 | 1 | O6CVH7 |
| 28 | 46 | 61.3 | 3411 | 1 | POLG_YEPV1 |
| 29 | 46 | 61.3 | 3411 | 1 | POLG_YEPV2 |
| 30 | 46 | 61.3 | 3411 | 1 | O91857 |
| 31 | 46 | 61.3 | 3411 | 2 | O98803 |

| | | | | | | |
|----|----|------|------|---|----------|--------------------|
| 32 | 46 | 61.3 | 3411 | 2 | O6DV88 | O6dv88 yellow feve |
| 33 | 46 | 61.3 | 3411 | 2 | O6J3P1 | O6j3p1 yellow feve |
| 34 | 46 | 61.3 | 3411 | 2 | O6PX46 | O6px46 yellow feve |
| 35 | 46 | 61.3 | 3411 | 2 | O89275 | O89275 yellow feve |
| 36 | 46 | 61.3 | 3411 | 2 | O89276 | O89276 yellow feve |
| 37 | 46 | 61.3 | 3411 | 2 | O89277 | O89277 yellow feve |
| 38 | 46 | 61.3 | 3411 | 2 | O89278 | O89278 yellow feve |
| 39 | 46 | 61.3 | 3411 | 2 | O9YRV3 | O9yrv3 yellow feve |
| 40 | 46 | 61.3 | 3411 | 2 | O9YVNO | O9yvno yellow feve |
| 41 | 46 | 61.3 | 3411 | 2 | O9YVNO | O9yvno yellow feve |
| 42 | 46 | 61.3 | 3411 | 2 | O9YVNO | O9yvno yellow feve |
| 43 | 45 | 60.0 | 142 | 2 | O6E881 | O6e881 aquifex aeo |
| 44 | 45 | 60.0 | 166 | 1 | MP36_PIG | P49931 sue scrofa |
| 45 | 45 | 60.0 | 174 | 2 | O9ZVE7 | O9zve7 arabidopsis |

ALIGNMENTS

RESULT 1
CP18_RABIT
ID CP18_RABIT STANDARD; PRT: 171 AA.
AC P25230;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DE 25-OCT-2004 (Rel. 45, Last annotation update)
DE Antimicrobial protein CAP18 precursor (18 kDa lipopolysaccharide-binding protein) (18 kDa cationic protein) (CAP18-A).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus;
OX NCBI_TaxID:9986;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 135-159.
RC TISSUE=Bone marrow;
RX MEDLINE=91354246; PubMed=1883348;
RA Larrick J.W., Morgan J.G., Palings I., Hirata M., Yen M.H.;
RT "Complementary DNA sequence of rabbit CAP18 -- a unique lipopolysaccharide binding protein.";
RL Biochem. Biophys. Res. Commun. 179:170-175(1991).
RN [2]
RP SEQUENCE OF 135-159, AND CHARACTERIZATION.
RX MEDLINE=94178952; PubMed=8132348;
RA Hirata M., Shimomura Y., Yoshida M., Morgan J.G., Palings I., Wilson D., Yen M.H., Wright S.C., Larrick J.W.;
RT "Characterization of a rabbit cationic protein (CAP18) with lipopolysaccharide-inhibitory activity.";
RL Infect. Immun. 62:1421-1426(1994).
RN [3]
RP SEQUENCE OF 135-154, AND CHARACTERIZATION.
RX MEDLINE=94075827; PubMed=8254193;
RA Larrick J.W., Hirata M., Zheng H., Zhong J., Bolin D., Cavallion J.-M., Warren H.S., Wright S.C.;
RT "A novel granulocyte-derived peptide with lipopolysaccharide-neutralizing activity.";
RL J. Immunol. 152:231-240(1994).
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=94148064; PubMed=8313956; DOI=10.1016/0014-5793(94)80395-1;
RA Tosi A., Scocchi M., Skerlavaj B., Gemmaro R.;
RT "Identification and characterization of a primary antibacterial domain in CAP18, a lipopolysaccharide binding protein from rabbit leukocytes.";
RL FEBS Lett. 339:108-112(1994).
RN [5]
RP STRUCTURE BY NMR OF 135-166.
RX MEDLINE=95377455; PubMed=7649303; DOI=10.1016/0014-5793(95)00792-8;
RA Chen C., Brock R., Luh F., Chou P.-J., Larrick J.W., Huang R.-F., Huang T.-H.;
RT "The solution structure of the active domain of CAP18 -- a lipopolysaccharide binding protein from rabbit leukocytes.";
RL FEBS Lett. 370:46-52(1995).

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OM protein - protein search, using SW model

Run on: May 2, 2005, 12:21:40 / Search time 9.30168 Seconds
(without alignments)
155.160 Million cell updates/sec

Title: US-09-642-744d-24

Perfect score: 75

Sequence: 1 RFRNKKIKKKKIG 15

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: 1: PIR.9:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 75 | 100.0 | 171 | 2 JQ1171 | 18K lipopolysaccha |
| 2 | 48 | 64.0 | 497 | 2 E90061 | hypothetical prote |
| 3 | 46 | 61.3 | 169 | 2 A82373 | polypeptide deform |
| 4 | 46 | 61.3 | 173 | 2 S70521 | cathelin-related p |
| 5 | 46 | 61.3 | 1163 | 1 GNMVY8 | genome polypotein |
| 6 | 46 | 61.3 | 3411 | 1 GNMVY | genome polypotein |
| 7 | 46 | 61.3 | 3411 | 1 GNMVY | genome polypotein |
| 8 | 46 | 61.3 | 3411 | 1 GNMVY | genome polypotein |
| 9 | 45 | 60.0 | 142 | 2 E70356 | hypothetical prote |
| 10 | 45 | 60.0 | 174 | 2 F84426 | hypothetical prote |
| 11 | 45 | 60.0 | 174 | 2 F84426 | hypothetical prote |
| 12 | 45 | 60.0 | 522 | 2 A95059 | hypothetical prote |
| 13 | 45 | 60.0 | 522 | 2 A95059 | hypothetical prote |
| 14 | 44 | 58.7 | 109 | 2 G64379 | type 1 site-specif |
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| 16 | 43.5 | 57.3 | 274 | 2 C69444 | hypothetical prote |
| 17 | 43 | 57.3 | 119 | 2 C90351 | conserved hypotet |
| 18 | 43 | 57.3 | 293 | 2 T04951 | hypothetical prote |
| 19 | 43 | 57.3 | 356 | 2 F64383 | hypothetical prote |
| 20 | 43 | 57.3 | 392 | 2 D96770 | hypothetical prote |
| 21 | 43 | 57.3 | 573 | 2 D90202 | hypothetical prote |
| 22 | 43 | 57.3 | 1631 | 1 SAZOK1 | methionyl-cRNA syn |
| 23 | 43 | 57.3 | 1639 | 2 S05603 | major mezozone su |
| 24 | 42 | 56.0 | 175 | 2 A24594 | probable major sur |
| 25 | 42 | 56.0 | 175 | 2 A24594 | hypothetical prote |
| 26 | 42 | 56.0 | 358 | 2 D95041 | hypothetical prote |
| 27 | 42 | 56.0 | 425 | 2 C97035 | uncharacterized pr |
| 28 | 42 | 56.0 | 476 | 2 D71108 | cysteine-tRNA lig |
| 29 | 42 | 56.0 | 524 | 1 S60406 | hypothetical prote |

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|----|----|------|------|----------|--------------------|
| 30 | 42 | 56.0 | 2038 | 2 A43742 | female sterile hom |
| 31 | 41 | 54.7 | 167 | 2 S25360 | signal recognition |
| 32 | 41 | 54.7 | 308 | 2 D64328 | hypothetical prote |
| 33 | 41 | 54.7 | 325 | 2 D81369 | hypothetical prote |
| 34 | 41 | 54.7 | 558 | 2 A64515 | type I restriction |
| 35 | 41 | 54.7 | 561 | 2 T41176 | hypothetical prote |
| 36 | 41 | 54.7 | 588 | 2 T45539 | moed protein limpo |
| 37 | 41 | 54.7 | 647 | 2 E64170 | ABC-type transport |
| 38 | 41 | 54.7 | 831 | 2 S44843 | K06H7.3 protein - |
| 39 | 41 | 54.7 | 851 | 2 T31520 | hypothetical prote |
| 40 | 40 | 53.3 | 96 | 2 F72228 | ribosomal protein |
| 41 | 40 | 53.3 | 127 | 2 A64466 | hypothetical prote |
| 42 | 40 | 53.3 | 133 | 2 B66796 | arsenate reductase |
| 43 | 40 | 53.3 | 176 | 2 B69519 | conserved hypotet |
| 44 | 40 | 53.3 | 233 | 2 S70531 | bdk2.11 protein pr |
| 45 | 40 | 53.3 | 241 | 2 G86355 | hypothetical prote |

ALIGNMENTS

RESULT 1
JQ1171
18K lipopolysaccharide-binding protein precursor - rabbit
N:Alternate names: 18K cationic protein
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 06-Dec-1996
C/Accession: JQ1171, PS0226
R:Latrick, J.W.; Morgan, J.G.; Palings, I.; Hirata, M.; Yen, M.H.
Biochem. Biophys. Res. Commun. 179, 170-175, 1991
A>Title: Complementary DNA sequence of rabbit Cap18-a unique lipopolysaccharide bindin
A/Reference number: JQ1171, MUID:91354246, PMID:1883348
A/Accession: JQ1171
A:Molecule type: mRNA
A:Residues: 1-171 <LAR>
A:Experimental source: bone marrow
A/Accession: PS0226
A:Molecule type: protein
A:Residues: 135-159, 'OIGQL' <LAR>
A>Note: 157-Asp was also found
C:Superfamily: cathelin; cystatin homology
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-171/Product: 18K lipopolysaccharide-binding protein #status predicted <MAT>

Query Match 100.0%; Score 75; DB 2; Length 171;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFRNKKIKKKKIG 15
Db 141 RFRNKKIKKKKIG 155

RESULT 2
E90061
hypothetical protein SA2351 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: E90061
R:Kuroda, M.; Ohca, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogi
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kato, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiratsugu, K.
Lancet 357, 1225-1240, 2001
A>Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A/Reference number: A89758; MUID:21311952; PMID:11418146
A/Accession: E90061
A/Status: preliminary
A:Molecule type: DNA
A:Residues: 1-497 <KUR>
A/Cross-references: UNIPROT:Q99R73; GB:BA000018; PID:g13702514; PIDN:BA843655.1; GSPDB:
A:Experimental source: strain N315
C/Genetic:
A:Gene: SA2351

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 2, 2005, 13:03:56 ; Search time 40.810 Seconds
(without alignments)

122.435 Million cell updates/sec

Title: US-09-642-744d-24

Sequence: 1 RKFRNKKIKKKIKG 15

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1426032 seqs, 333106140 residues

Total number of hits satisfying chosen parameters: 1426032

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

Published Applications AA:*
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15: /cgn2_6/ptodata/1/pubppa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubppa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubppa/US10_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the total score distribution,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 2 | 75 | 100.0 | 37 | 14 | US-10-060-102-5 |
| 3 | 75 | 100.0 | 37 | 15 | US-10-721-839-5 |
| 4 | 75 | 100.0 | 37 | 16 | US-10-344-709C-15 |
| 5 | 75 | 100.0 | 171 | 16 | US-10-344-709C-7 |
| 6 | 48 | 64.0 | 439 | 9 | US-09-815-242-5696 |
| 7 | 48 | 64.0 | 497 | 14 | US-10-358-917-14 |
| 8 | 48 | 64.0 | 497 | 15 | US-10-283-1122A-43955 |
| 9 | 47 | 62.7 | 443 | 16 | US-10-767-701-44345 |
| 10 | 47 | 62.7 | 881 | 15 | US-10-282-122A-52284 |
| 11 | 46 | 61.3 | 31 | 17 | US-10-399-442A-2 |
| 12 | 46 | 61.3 | 32 | 16 | US-10-344-709C-1 |
| 13 | 46 | 61.3 | 35 | 13 | US-10-205-150-1 |

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| 14 | 46 | 61.3 | 36 | 14 | US-10-269-171A-2 | Sequence 2, Appl1 |
| 15 | 46 | 61.3 | 36 | 17 | US-10-470-048B-599 | Sequence 599, App |
| 16 | 46 | 61.3 | 39 | 14 | US-10-060-102-1 | Sequence 1, Appl1 |
| 17 | 46 | 61.3 | 39 | 15 | US-10-721-839-1 | Sequence 1, Appl1 |
| 18 | 46 | 61.3 | 39 | 15 | US-10-721-839-5 | Sequence 5, Appl1 |
| 19 | 46 | 61.3 | 173 | 16 | US-10-344-709C-5 | Sequence 58098, A |
| 20 | 46 | 61.3 | 1111 | 16 | US-10-282-122A-58098 | Sequence 22, Appl1 |
| 21 | 45 | 60.0 | 522 | 15 | US-10-398-186-22 | Sequence 73834, A |
| 22 | 45 | 60.0 | 522 | 17 | US-10-282-122A-73834 | Sequence 878, App |
| 23 | 44 | 58.7 | 81 | 15 | US-10-472-928-878 | Sequence 274937, A |
| 24 | 44 | 58.7 | 90 | 16 | US-10-424-599-274937 | Sequence 111957, A |
| 25 | 44 | 58.7 | 504 | 15 | US-10-437-963-111957 | Sequence 67643, A |
| 26 | 43 | 57.3 | 51 | 15 | US-10-425-114-67643 | Sequence 264915, A |
| 27 | 43 | 57.3 | 59 | 15 | US-10-424-599-264915 | Sequence 243585, A |
| 28 | 43 | 57.3 | 338 | 15 | US-10-424-599-243585 | Sequence 6, Appl1 |
| 29 | 43 | 57.3 | 449 | 15 | US-10-155-435-64900 | Sequence 54900, A |
| 30 | 43 | 57.3 | 623 | 15 | US-10-425-114-54900 | Sequence 215078, A |
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| 32 | 43 | 57.3 | 1639 | 14 | US-10-424-599-208110 | Sequence 148381, A |
| 33 | 42 | 56.0 | 60 | 16 | US-10-087-464-10 | Sequence 536, App |
| 34 | 42 | 56.0 | 358 | 17 | US-10-437-963-1148381 | Sequence 250653, A |
| 35 | 41 | 54.7 | 67 | 15 | US-10-424-599-250653 | Sequence 181959, A |
| 36 | 41 | 54.7 | 108 | 15 | US-10-424-599-181959 | Sequence 264276, A |
| 37 | 41 | 54.7 | 129 | 15 | US-10-424-599-264276 | Sequence 226719, A |
| 38 | 41 | 54.7 | 136 | 15 | US-10-424-599-226719 | Sequence 34, Appl1 |
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| 40 | 41 | 54.7 | 161 | 16 | US-10-767-701-60391 | Sequence 2, Appl1 |
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| 42 | 41 | 54.7 | 178 | 15 | US-10-188-840-2 | Sequence 170068, A |
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ALIGNMENTS

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Sequence 1, Application US/10111433
Publication No. US20030054422A1
GENERAL INFORMATION:
APPLICANT: UNILEVER, PLC
TITLE OF INVENTION: Lipopolysaccharide Immunoassay and Test Device
FILE REFERENCE: Lipopolysaccharide Immunoassay
CURRENT APPLICATION NUMBER: US/10/131,433
CURRENT FILING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: US/09/545,180
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 32
TYPE: PRT
ORGANISM: Lipine
US-10-131-433-1

Query Match 100.0%; Score 75; DB 14; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.00067;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKFRNKKIKKKIKG 15
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Db 7 RKFRNKKIKKKIKG 21

RESULT 2
US-10-060-102-5
Sequence 5, Application US/10060102
Publication No. US20030028282A1
GENERAL INFORMATION:
APPLICANT: MAURY, WENDY
APPLICANT: STABLETON, JACK

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:18:40 ; Search time 14.2458 Seconds

(without alignments)
78.601 Million cell updates/sec

Title: US-09-642-744D-24

Perfect score: 75

Sequence: 1 RKRNRKIKKXKIG 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 5 | 51 | 68.0 | 16 | 1 | US-08-313-681A-11 |
| 6 | 51 | 68.0 | 16 | 3 | US-09-322-911-11 |
| 7 | 47 | 62.7 | 18 | 4 | US-09-525-269A-10 |
| 8 | 46 | 61.3 | 33 | 5 | PCT-US95-12080-4 |
| 9 | 46 | 61.3 | 3421 | 4 | US-09-452-638-53 |
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| 23 | 40 | 53.3 | 343 | 3 | US-09-069-226-28 |
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| 25 | 40 | 53.3 | 524 | 4 | US-09-248-796A-18625 |
| 26 | 40 | 53.3 | 898 | 4 | US-09-585-858-37 |
| 27 | 40 | 53.3 | 898 | 4 | US-10-270-878-37 |

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| 28 | 40 | 53.3 | 956 | 4 | US-09-107-532A-5007 | Sequence 5007, Ap |
| 29 | 39 | 52.0 | 18 | 1 | US-07-725-331-29 | Sequence 29, Appl |
| 30 | 39 | 52.0 | 18 | 5 | PCT-US91-05047-29 | Sequence 29, Appl |
| 31 | 39 | 52.0 | 74 | 4 | US-09-248-796A-25957 | Sequence 25957, A |
| 32 | 39 | 52.0 | 87 | 4 | US-09-248-796A-24551 | Sequence 24551, A |
| 33 | 39 | 52.0 | 96 | 4 | US-09-732-210-707 | Sequence 707, App |
| 34 | 39 | 52.0 | 154 | 4 | US-09-248-796A-27970 | Sequence 27970, A |
| 35 | 39 | 52.0 | 166 | 4 | US-09-270-767-51496 | Sequence 36279, A |
| 36 | 39 | 52.0 | 231 | 4 | US-09-248-796A-14758 | Sequence 51496, A |
| 37 | 39 | 52.0 | 306 | 3 | US-09-134-001C-4678 | Sequence 14758, A |
| 38 | 39 | 52.0 | 378 | 4 | US-09-498-520A-44 | Sequence 4678, Ap |
| 39 | 39 | 52.0 | 395 | 3 | US-09-134-001C-3723 | Sequence 44, Appl |
| 40 | 39 | 52.0 | 396 | 4 | US-09-502-540-15124 | Sequence 3723, Ap |
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| 42 | 39 | 52.0 | 672 | 3 | US-09-621-855-4 | Sequence 4, Appl |
| 43 | 39 | 52.0 | 817 | 4 | US-09-710-279-50 | Sequence 4, Appl |
| 44 | 39 | 52.0 | 817 | 4 | US-09-710-279-1528 | Sequence 50, Appl |
| 45 | 39 | 52.0 | 817 | 4 | US-09-710-279-1528 | Sequence 1528, Ap |

ALIGNMENTS

RESULT 1
US-08-313-681A-7
Sequence 7, Application US/08313681A
Patent No. 5618675
GENERAL INFORMATION:
APPLICANT: Larrick, James W.
APPLICANT: Wright, Susan C.
APPLICANT: Hirata, Mishimasa
TITLE OF INVENTION: Human Cationic Proteins Having
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESSES:
ADDRESSER: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Steuart Tower,
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,681A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15325-9-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Region
LOCATION: 23
OTHER INFORMATION: /note= "Xaa is Asp or Lys"
FEATURE:
NAME/KEY: Region
LOCATION: 26
OTHER INFORMATION: /note= "Xaa is a Gln or Ile"
FEATURE:

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:17:55 ; Search time 52.5838 Seconds

(without alignments)
110.327 Million cell updates/sec

Title: US-09-642-744d-24

Sequence: 1 RKFRKKIKKKKIG 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq16Dec04:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 4 | 75 | 100.0 | 21 | 4 AAB70666 | Aab70666 Lupine RC |
| 5 | 75 | 100.0 | 21 | 4 AAB70670 | Aab70670 Lupine RC |
| 6 | 75 | 100.0 | 22 | 4 AAB70668 | Aab70668 Lupine RC |
| 7 | 75 | 100.0 | 24 | 6 AAB34416 | Aae34416 Rabbit RC |
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| 9 | 75 | 100.0 | 24 | 8 ADK70764 | Aae34416 Rabbit RC |
| 10 | 75 | 100.0 | 26 | 6 AAE34418 | Aae34418 Rabbit CA |
| 11 | 75 | 100.0 | 26 | 6 AAE34417 | Aae34417 Rabbit CA |
| 12 | 75 | 100.0 | 26 | 6 AAE34419 | Aae34419 Rabbit CA |
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| 19 | 75 | 100.0 | 32 | 8 ADK70761 | Aab70761 Rabbit CA |
| 20 | 75 | 100.0 | 37 | 4 AAB70665 | Aab70665 Lupine RC |
| 21 | 75 | 100.0 | 37 | 5 ABB07711 | Abb07711 Antimicro |
| 22 | 75 | 100.0 | 37 | 5 ABB53272 | Abb53272 Sheep nat |
| 23 | 75 | 100.0 | 38 | 4 AAB51193 | Aab51193 E. coli A |
| 24 | 75 | 100.0 | 142 | 8 ADK70796 | Adk70796 Rabbit CA |
| 25 | 75 | 100.0 | 171 | 5 ABB07703 | Abb07703 Rabbit pe |

| | | | | | |
|----|----|------|-----|------------|--------------------|
| 26 | 69 | 92.0 | 20 | 8 ADK70765 | Adk70765 Rabbit CA |
| 27 | 51 | 68.0 | 16 | 2 AAB45673 | Aab45673 RNP hepa |
| 28 | 51 | 68.0 | 16 | 3 AAB07905 | Aab07905 Heparin-b |
| 29 | 48 | 64.0 | 15 | 4 AAB70672 | Aab70672 Lupine RC |
| 30 | 48 | 64.0 | 17 | 4 AAB70673 | Aab70673 Lupine RC |
| 31 | 48 | 64.0 | 439 | 4 AAB70673 | Aab70673 Lupine RC |
| 32 | 48 | 64.0 | 497 | 6 AAB16031 | Aab16031 Staphyloc |
| 33 | 48 | 64.0 | 497 | 6 AAB16031 | Aab16031 Staphyloc |
| 34 | 48 | 64.0 | 500 | 6 AAB16031 | Aab16031 Staphyloc |
| 35 | 47 | 62.7 | 18 | 2 AAB72616 | Abm72616 Staphyloc |
| 36 | 47 | 62.7 | 18 | 2 AAB72616 | Abm72616 Staphyloc |
| 37 | 47 | 62.7 | 18 | 2 AAB72616 | Abm72616 Staphyloc |
| 38 | 46 | 61.3 | 31 | 5 AAB07697 | Aab07697 Murine ca |
| 39 | 46 | 61.3 | 32 | 5 AAB07697 | Aab07697 Murine ca |
| 40 | 46 | 61.3 | 33 | 2 AAB94449 | Aab94449 Mouse ant |
| 41 | 46 | 61.3 | 35 | 8 AAB84033 | Abm84033 Murine ca |
| 42 | 46 | 61.3 | 36 | 4 AAG66421 | Aag66421 Mouse cat |
| 43 | 46 | 61.3 | 36 | 5 AAU09819 | Aau09819 Mouse cat |
| 44 | 46 | 61.3 | 36 | 5 AAG31966 | Agg31966 Mouse cat |
| 45 | 46 | 61.3 | 36 | 5 AAG31663 | Agg31663 Mouse cat |

ALIGNMENTS

RESULT 1
AAB70671
ID AAB70671 standard; peptide; 15 AA.

AC AAB70671;

DT 15-MAY-2001 (first entry)

DE Lupine RCAP 18 cathelicidin derived antimicrobial peptide SEQ ID NO:24.

KW Ovine; SNAP29; lupine; RCAP 18; cathelicidin; antimicrobial;

KW bactericidal; antibiotic; antiviral; microbial growth inhibitor;

KW proliferation inhibitor; gene therapy; Pseudomonas aeruginosa;

OS Burkholderia cepacia; Alcaligenes; Xanthomonas.

OS Oryctolagus cuniculus.

PN WO200112668-A1.

PD 22-FEB-2001.

PF 18-AUG-2000; 2000WO-US022781.

PR 18-AUG-1999; 99US-0149886P.

PA (TOWA) UNIV TOWA RES FOUND.

PA (REGC) UNIV CALIFORNIA.

PI Tack BE, Mccray P, Welsh M, Travis SM, Lehrer R;

DR WPI; 2001-234911/24.

PT New antimicrobial peptides useful as antibiotics for inhibiting growth

PT and proliferation of microbes, and for treating microbial infections.

PS Claim 1, Page 103; 137pp; English.

XX AAB70648 to AAB70675 represent antimicrobial peptides (I), of which

XX AAB70648 to AAB70664, AAB70674 and AAB70675 are derived from the ovine

XX SMAP 29 cathelicidin family peptide, and AAB70665 to AAB70673 are derived

XX from the lupine RCAP 18 cathelicidin family peptide. (I) have antibiotic,

XX antimicrobial and antiviral activities, and can be used as microbial

XX growth and proliferation inhibitors and in gene therapy. (I) are useful

XX for inhibiting microbial growth in an environment capable of sustaining

XX such growth, for inhibiting microbial growth or strain in a host, and

XX inhibiting the growth of drug-resistant microbial strains such as

XX Pseudomonas aeruginosa, Burkholderia cepacia, Alcaligenes and Xanthomonas

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:21:40 ; Search time 13.0223 Seconds

(without alignments)
155.160 Million cell updates/sec

Title: US-09-642-744D-23

Sequence: 1 LRKFRNKIKKIKGKIQIG 21

Scoring table: BIOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database:

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 104 | 100.0 | 171 | 2 J01171 | 18K lipopolysaccha |
| 2 | 65 | 62.5 | 173 | 2 S70521 | cathelin-related p |
| 3 | 60 | 57.7 | 324 | 2 T07982 | probable choline-p |
| 4 | 60 | 57.7 | 326 | 2 T07983 | choline-phosphate |
| 5 | 57 | 54.8 | 329 | 2 T07981 | probable choline-p |
| 6 | 57 | 54.8 | 331 | 2 T07980 | probable choline-p |
| 7 | 54 | 51.9 | 332 | 2 H84730 | probable phospholi |
| 8 | 50 | 48.1 | 354 | 2 B75003 | hypothetical prote |
| 9 | 50 | 48.1 | 519 | 2 T51496 | hypothetical prote |
| 10 | 50 | 48.1 | 663 | 2 D97047 | DNA ligase (NAD de |
| 11 | 50 | 48.1 | 1163 | 2 GNMVY8 | genome polyprotein |
| 12 | 50 | 48.1 | 3411 | 1 GNMVY | genome polyprotein |
| 13 | 49 | 47.1 | 3411 | 1 GNMVY | genome polyprotein |
| 14 | 49 | 47.1 | 142 | 2 E70356 | synthetaxin-like |
| 15 | 49 | 47.1 | 259 | 2 G01485 | synthetaxin-like |
| 16 | 49 | 47.1 | 288 | 2 G01485 | synthetaxin-like |
| 17 | 49 | 47.1 | 298 | 2 A38141 | neuron-specific an |
| 18 | 49 | 47.1 | 829 | 2 T33744 | hypothetical prote |
| 19 | 48 | 46.2 | 117 | 1 H71166 | hypothetical prote |
| 20 | 48 | 46.2 | 117 | 2 E75065 | hypothetical prote |
| 21 | 48 | 46.2 | 152 | 2 C72227 | conserved hypotet |
| 22 | 48 | 46.2 | 288 | 2 J00136 | synapocanalin I - |
| 23 | 48 | 46.2 | 293 | 2 T04951 | synthetaxin 1B - |
| 24 | 48 | 46.2 | 293 | 2 T04951 | synthetaxin 1B - |
| 25 | 48 | 46.2 | 497 | 2 E90061 | hypothetical prote |
| 26 | 48 | 46.2 | 818 | 2 P88819 | endopeptidase (imp |
| 27 | 47.5 | 45.7 | 274 | 2 C69444 | conserved hypotet |
| 28 | 47 | 45.2 | 166 | 2 S41731 | antibacterial prot |
| 29 | 47 | 45.2 | 174 | 2 P84426 | hypothetical prote |

| | | | | | |
|----|------|------|------|----------|--------------------|
| 30 | 47 | 45.2 | 188 | 1 F6494 | conserved hypotet |
| 31 | 47 | 45.2 | 249 | 2 E75181 | ribonuclease ph (r |
| 32 | 47 | 45.2 | 507 | 2 C82901 | conserved hypotet |
| 33 | 47 | 45.2 | 573 | 2 D90202 | methionyl-tRNA syn |
| 34 | 47 | 45.2 | 1631 | 1 SAZOK1 | major merozoite su |
| 35 | 47 | 45.2 | 1639 | 2 S05603 | probable major sur |
| 36 | 47 | 45.2 | 1640 | 2 A24594 | signal recognition |
| 37 | 46.5 | 44.7 | 376 | 2 S25360 | N-acetylornithine |
| 38 | 46.5 | 44.7 | 376 | 2 G70301 | polypeptide deform |
| 39 | 46 | 44.2 | 169 | 2 A82373 | hypothetical prote |
| 40 | 46 | 44.2 | 362 | 2 T22204 | iron-sulfur cluste |
| 41 | 46 | 44.2 | 369 | 2 F82333 | hypothetical prote |
| 42 | 46 | 44.2 | 392 | 2 B85363 | hypothetical prote |
| 43 | 46 | 44.2 | 533 | 2 T06153 | hypothetical prote |
| 44 | 46 | 44.2 | 1156 | 2 B70356 | chromosome assembl |
| 45 | 46 | 44.2 | 1236 | 2 T18459 | hypothetical prote |

ALIGNMENTS

RESULT 1

J01171 18K lipopolysaccharide-binding protein precursor - rabbit

N/Alternate names: 18K cationic protein

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 06-Dec-1996

C/Accession: J01171, PS0226

R/Larrick, J.W.; Morgan, J.G.; Palling, I.; Hirata, M.; Yen, M.H.

Biochem. Biophys. Res. Commun. 179, 170-175, 1991

A/Title: Complementary DNA sequence of rabbit CAP18-a unique lipopolysaccharide binding

A/Reference number: J01171, M01D:9154246, PMID:1883348

A/Accession: J01171

A/Molecule type: mRNA

A/Residues: 1-171 <LAAR>

A/Experimental source: bone marrow

A/Accession: PS0226

A/Molecule type: protein

A/Residues: 135-159, 'OTGOL' <LA2>

A/Note: 157-Asp was also found

C/Superfamily: cathelin; cystatin homology

F/1-29/Domain: signal sequence #status predicted <SIG>

F/30-171/Product: 18K lipopolysaccharide-binding protein #status predicted <MAT>

Query Match Best Local Similarity 100.0%; Score 104; DB 2; Length 171;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LRKFRNKIKKIKGKIQIG 21

Db 140 LRKFRNKIKKIKGKIQIG 160

RESULT 2

S70521 cathelin-related protein precursor - mouse

C/Species: Mus musculus (house mouse)

C/Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004

C/Accession: S70521

R/Popova, A.B.; Zinovjeva, M.V.; Vlaser, J.W.M.; Zijlman, J.M.J.M.; Fibbe, W.E.; Bel

FEBS Lett. 391, 5-8, 1996

A/Title: A novel murine cathelin-like protein expressed in bone marrow.

A/Reference number: S70521, M01D:96326596, PMID:8706928

A/Accession: S70521

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-173 <POP>

A/Cross-references: UNIPROT:P51437; EMBL:X94353; NID:91177533; PIDN:CAA64078.1; PID:911

F/1-23/Domain: signal sequence #status predicted <SIG>

F/24-144/Domain: propeptide #status predicted <PRO>

F/145-173/Product: cathelin-related protein #status predicted <MAT>

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:18:40 ; Search time 19.9441 Seconds
(without alignments)

78,601 Million cell updates/sec

Title: US-09-642-744D-23

Perfect score: 104

Sequence: 1 LRKFRNKIKKXIGKXIGK 21

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCUS.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---------------------|
| 1 | 104 | 100.0 | 171 | 1 | US-08-313-681A-4 |
| 2 | 104 | 100.0 | 171 | 1 | US-09-322-911-4 |
| 3 | 92 | 88.5 | 29 | 1 | US-08-313-681A-7 |
| 4 | 92 | 88.5 | 29 | 3 | US-09-322-911-7 |
| 5 | 65 | 62.5 | 33 | 5 | PCT-US95-12080-4 |
| 6 | 60 | 57.7 | 326 | 4 | US-09-735-846-25 |
| 7 | 57 | 54.8 | 329 | 4 | US-09-735-846-24 |
| 8 | 57 | 54.8 | 331 | 4 | US-09-735-846-23 |
| 9 | 55 | 52.9 | 16 | 1 | US-08-313-681A-11 |
| 10 | 55 | 52.9 | 16 | 3 | US-09-322-911-11 |
| 11 | 52 | 50.0 | 194 | 4 | US-09-735-846-6 |
| 12 | 52 | 50.0 | 363 | 4 | US-09-735-846-20 |
| 13 | 50 | 48.1 | 3421 | 4 | US-09-452-638-53 |
| 14 | 49 | 47.1 | 190 | 1 | US-08-393-985-25 |
| 15 | 49 | 47.1 | 259 | 4 | US-09-509-738C-25 |
| 16 | 49 | 47.1 | 263 | 1 | US-08-393-985-23 |
| 17 | 49 | 47.1 | 285 | 1 | US-08-393-985-2 |
| 18 | 49 | 47.1 | 288 | 1 | US-08-337-602-4 |
| 19 | 49 | 47.1 | 288 | 3 | US-08-558-135-4 |
| 20 | 49 | 47.1 | 288 | 3 | US-08-819-286-3 |
| 21 | 49 | 47.1 | 434 | 4 | US-09-489-039A-8456 |
| 22 | 48 | 46.2 | 104 | 4 | US-09-735-846-8 |
| 23 | 48 | 46.2 | 158 | 4 | US-08-356-397-4 |
| 24 | 48 | 46.2 | 288 | 1 | US-08-356-397-2 |
| 25 | 48 | 46.2 | 288 | 1 | US-08-393-985-4 |
| 26 | 48 | 46.2 | 288 | 4 | US-09-509-738C-26 |
| 27 | 48 | 46.2 | 672 | 3 | US-09-040-843-4 |

| | | | | | | |
|----|------|------|-----|---|----------------------|-------------------|
| 28 | 48 | 46.2 | 672 | 3 | US-09-621-855-4 | Sequence 4, Appl |
| 29 | 48 | 46.2 | 866 | 3 | US-09-040-843-2 | Sequence 2, Appl |
| 30 | 48 | 46.2 | 866 | 3 | US-09-621-855-2 | Sequence 2, Appl |
| 31 | 47 | 45.2 | 18 | 4 | US-09-525-269A-10 | Sequence 10, Appl |
| 32 | 47 | 45.2 | 90 | 4 | US-09-489-039A-11599 | Sequence 11599, A |
| 33 | 47 | 45.2 | 141 | 4 | US-09-270-767-42264 | Sequence 42264, A |
| 34 | 47 | 45.2 | 306 | 3 | US-09-134-001C-4678 | Sequence 4678, Ap |
| 35 | 47 | 45.2 | 502 | 4 | US-09-328-352-6968 | Sequence 6968, Ap |
| 36 | 46.5 | 44.7 | 343 | 2 | US-08-599-171A-28 | Sequence 28, Appl |
| 37 | 46.5 | 44.7 | 343 | 2 | US-08-646-590B-28 | Sequence 28, Appl |
| 38 | 46.5 | 44.7 | 343 | 3 | US-09-069-326-28 | Sequence 28, Appl |
| 39 | 46.5 | 44.7 | 343 | 3 | US-09-412-184-28 | Sequence 28, Appl |
| 40 | 46 | 44.2 | 22 | 3 | US-08-940-095-74 | Sequence 28, Appl |
| 41 | 46 | 44.2 | 22 | 3 | US-08-940-095-93 | Sequence 28, Appl |
| 42 | 46 | 44.2 | 22 | 3 | US-08-940-093-74 | Sequence 28, Appl |
| 43 | 46 | 44.2 | 22 | 3 | US-08-940-093-93 | Sequence 28, Appl |
| 44 | 46 | 44.2 | 22 | 3 | US-08-940-096-74 | Sequence 28, Appl |
| 45 | 46 | 44.2 | 22 | 3 | US-08-940-096-93 | Sequence 28, Appl |

ALIGNMENTS

RESULT 1
US-08-313-681A-4
Sequence 4, Appl
Patent No. 5618675
GENERAL INFORMATION:
APPLICANT: Larrick, James W.
APPLICANT: Wright, Susan C.
APPLICANT: Hirata, Mitsuhiro
TITLE OF INVENTION: Human Cationic Proteins Having
NUMBER OF SEQUENCES: 30
TITLE OF INVENTION: Lipopolysaccharide Binding and Anti-Coagulant Activity
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,681A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15325-9-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 171 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-313-681A-4
Query Match 100.0%; Score 104; DB 1; Length 171;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 LRKFRNKIKKXIGKXIGK 21
140 LRKFRNKIKKXIGKXIGK 160

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:17:55 ; Search time 73.6173 Seconds
(without alignments)
110.327 Million cell updates/sec

Title: US-09-642-744D-23

Perfect score: 104

Sequence: 1 LRKFRNKIKKKIKGKIQG 21

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
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2: geneeqp19908:*
3: geneeqp20008:*
4: geneeqp2001s:*
5: geneeqp2002s:*
6: geneeqp2003as:*
7: geneeqp2003bs:*
8: geneeqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|-------|-------------|--------|----|----------|-------------|
| 1 | 104 | 100.0 | 21 | 4 | AAB70670 | Lupine RC |
| 2 | 104 | 100.0 | 32 | 3 | AAB28486 | Rabbit 11 |
| 3 | 104 | 100.0 | 32 | 8 | ADK70761 | Rabbit CA |
| 4 | 104 | 100.0 | 37 | 4 | AAB70665 | Lupine RC |
| 5 | 104 | 100.0 | 37 | 5 | ABB07711 | Artimicro |
| 6 | 104 | 100.0 | 37 | 5 | ABP53272 | Sheep nat |
| 7 | 104 | 100.0 | 38 | 4 | AAB51193 | E. coli A |
| 8 | 104 | 100.0 | 142 | 8 | ADK70796 | Rabbit CA |
| 9 | 104 | 100.0 | 171 | 5 | ABB07703 | Rabbit pe |
| 10 | 94 | 90.4 | 26 | 6 | AAE34418 | Rabbit CA |
| 11 | 94 | 90.4 | 26 | 6 | AAE34417 | Rabbit CA |
| 12 | 94 | 90.4 | 26 | 6 | AAE34419 | Rabbit CA |
| 13 | 94 | 90.4 | 26 | 6 | AAE34420 | Rabbit CA |
| 14 | 94 | 90.4 | 26 | 8 | ADK70762 | Rabbit CA |
| 15 | 93 | 89.4 | 19 | 4 | AAB70669 | Lupine RC |
| 16 | 93 | 89.4 | 22 | 4 | AAB70668 | Lupine RC |
| 17 | 93 | 89.4 | 24 | 6 | AAE34416 | Rabbit RC |
| 18 | 93 | 89.4 | 24 | 8 | ADK70763 | Rabbit RC |
| 19 | 93 | 89.4 | 26 | 6 | AAE34421 | Rabbit CA |
| 20 | 92 | 88.5 | 29 | 2 | AAR45671 | N termimu |
| 21 | 92 | 88.5 | 29 | 3 | AAB07903 | Purative |
| 22 | 89 | 85.6 | 24 | 8 | ADK70764 | Rabbit CA |
| 23 | 79 | 76.0 | 18 | 4 | AAB70667 | Lupine RC |
| 24 | 79 | 76.0 | 21 | 4 | AAB70666 | Lupine RC |
| 25 | 75 | 72.1 | 15 | 4 | AAB70671 | Lupine RC |

| | | | | | | |
|----|----|------|-----|---|----------|-----------|
| 26 | 73 | 70.2 | 15 | 4 | AAB70672 | Lupine RC |
| 27 | 73 | 70.2 | 17 | 4 | AAB70673 | Lupine RC |
| 28 | 73 | 70.2 | 20 | 8 | ADK70765 | Rabbit CA |
| 29 | 65 | 62.5 | 31 | 5 | AAO15559 | Murine ca |
| 30 | 65 | 62.5 | 32 | 5 | ABO7697 | Murine ca |
| 31 | 65 | 62.5 | 33 | 2 | AAR94449 | Mouse ant |
| 32 | 65 | 62.5 | 39 | 5 | ABP53268 | Mouse nat |
| 33 | 65 | 62.5 | 173 | 5 | ABBO7701 | Murine ca |
| 34 | 60 | 57.7 | 324 | 8 | ADJ49167 | Oil-aseoc |
| 35 | 60 | 57.7 | 326 | 6 | ADA06238 | Rape chol |
| 36 | 60 | 57.7 | 326 | 8 | ADJ49168 | Oil-aseoc |
| 37 | 59 | 57.7 | 326 | 8 | ADJ49169 | Brasica |
| 38 | 59 | 56.7 | 36 | 4 | AAE64421 | Mouse cat |
| 39 | 59 | 56.7 | 36 | 5 | AAU09819 | Mouse cat |
| 40 | 59 | 56.7 | 36 | 5 | ABG31966 | Mouse cat |
| 41 | 59 | 56.7 | 36 | 5 | ABG31663 | Mouse cat |
| 42 | 59 | 56.7 | 36 | 5 | AAU76940 | Mouse cat |
| 43 | 59 | 56.7 | 36 | 6 | ABP58358 | Mouse cat |
| 44 | 59 | 56.7 | 36 | 8 | ADJ51139 | Murine ca |
| 45 | 57 | 54.8 | 329 | 6 | ADA06237 | Rape chol |

ALIGNMENTS

RESULT 1
AAB70670
ID AAB70670 standard; peptide; 21 AA.
XX
AC AAB70670;
XX
DT 15-MAY-2001 (first entry)
XX
DE Lupine RCAP 18 cathelicidin derived antimicrobial peptide SEQ ID NO:23.
XX
XX Ovine; SWAP29; lupine; RCAP 18; cathelicidin; antimicrobial;
XX bactericidal; antibiotic; antiviral; microbial growth inhibitor;
XX proliferation inhibitor; gene therapy; Pseudomonas aeruginosa;
XX Burkholderia cepacia; Alcaligenes; Xanthomonas.
XX
XX Oryzococcus cuniculus.
XX
XX WO200112668-A1.
XX
XX 22-FEB-2001.
XX
PF 18-AUG-2000; 2000MO-US022781.
XX
PR 18-AUG-1999; 99US-0149886P.
XX
PR (IOWA) UNIV IOWA RES FOUND.
XX (REGC) UNIV CALIFORNIA.
XX
PI Tack BE, Mccray P, Welsh M, Travis SM, Lehrer R;
XX WPI; 2001-234911/24.
XX
PT New antimicrobial peptides useful as antibiotics for inhibiting growth
XX and proliferation of microbes, and for treating microbial infections.
XX
XX Claim 1; Page 103; 137pp; English.
XX
XX AAB70648 to AAB70675 represent antimicrobial peptides (I), of which
XX AAB70648 to AAB70664, AAB70674 and AAB70675 are derived from the ovine
XX SMAP 29 cathelicidin family peptide, and AAB70665 to AAB70673 are derived
XX from the lupine RCAP 18 cathelicidin family peptide. (I) have antibiotic,
XX antimicrobial and antiviral activities, and can be used as microbial
XX growth and proliferation inhibitors and in gene therapy. (II) are useful
XX for inhibiting microbial growth in an environment capable of sustaining
XX such growth, for inhibiting microbial growth or strain in a host, and
XX inhibiting the growth of drug-resistant microbial strains such as
XX Pseudomonas aeruginosa, Burkholderia cepacia, Alcaligenes and Xanthomonas

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:17:06 ; Search time 59.2821 Seconds

(without alignments)
164.122 Million cell updates/sec

Title: US-09-642-744D-22

Sequence: 1 LRRFRNKKIKKKIKGKI 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: uniprot_sprot.*
2: uniprot_tramb1.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 93 | 100.0 | 171 | 1 | CP18 RABIT |
| 2 | 64 | 68.8 | 173 | 1 | CRAN_MOUSE |
| 3 | 61 | 65.6 | 511 | 2 | Q7P8L9 |
| 4 | 57 | 61.3 | 171 | 2 | Q71KM5 |
| 5 | 55 | 59.1 | 324 | 2 | Q42621 |
| 6 | 55 | 59.1 | 326 | 2 | Q42622 |
| 7 | 54 | 58.1 | 508 | 1 | YU13 FUSNN |
| 8 | 53 | 57.0 | 170 | 2 | Q9GLV5 |
| 9 | 53 | 57.0 | 3787 | 2 | Q811Z6 |
| 10 | 52 | 55.9 | 329 | 2 | Q42620 |
| 11 | 52 | 55.9 | 331 | 2 | Q42619 |
| 12 | 52 | 55.9 | 362 | 2 | Q9BPM9 |
| 13 | 52 | 55.9 | 1111 | 1 | YJEP HAEIN |
| 14 | 50 | 53.8 | 224 | 2 | Q6W9J9 |
| 15 | 50 | 53.8 | 235 | 2 | Q6W9J1 |
| 16 | 50 | 53.8 | 299 | 2 | Q7P6A4 |
| 17 | 50 | 53.8 | 668 | 2 | Q891I0 |
| 18 | 50 | 53.8 | 811 | 1 | COAT GMDNV |
| 19 | 50 | 53.8 | 1901 | 2 | Q86LFG |
| 20 | 49.5 | 53.2 | 420 | 2 | Q86LFG |
| 21 | 49 | 52.7 | 133 | 2 | Q86LFG |
| 22 | 49 | 52.7 | 142 | 2 | Q66881 |
| 23 | 49 | 52.7 | 332 | 2 | Q92V56 |
| 24 | 49 | 52.7 | 332 | 2 | Q92V56 |
| 25 | 49 | 52.7 | 400 | 2 | Q89295 |
| 26 | 49 | 52.7 | 400 | 2 | Q89297 |
| 27 | 49 | 52.7 | 400 | 2 | Q89299 |
| 28 | 49 | 52.7 | 400 | 2 | Q89304 |
| 29 | 49 | 52.7 | 400 | 2 | Q89311 |
| 30 | 49 | 52.7 | 400 | 2 | Q89315 |
| 31 | 49 | 52.7 | 400 | 2 | Q89317 |

| | | | | | | |
|----|----|------|------|---|-------------|----------------------|
| 32 | 49 | 52.7 | 425 | 2 | P96200 | P96200 bacteroides |
| 33 | 49 | 52.7 | 598 | 2 | Q48537 | Q48537 lactobacill |
| 34 | 49 | 52.7 | 778 | 2 | P89915 | P89915 yellow feve |
| 35 | 49 | 52.7 | 778 | 2 | Q77X62 | Q77X62 yellow feve |
| 36 | 49 | 52.7 | 778 | 2 | Q77X64 | Q77X64 yellow feve |
| 37 | 49 | 52.7 | 778 | 2 | Q9W9B8 | Q9W9B8 yellow feve |
| 38 | 49 | 52.7 | 1163 | 1 | POLG_YEYFV8 | P29165 yellow feve |
| 39 | 49 | 52.7 | 3411 | 1 | POLG_YEYFV1 | P03314 Y genome feve |
| 40 | 49 | 52.7 | 3411 | 2 | POLG_YEYFV2 | P19901 Y genome po |
| 41 | 49 | 52.7 | 3411 | 2 | Q91857 | Q91857 yellow feve |
| 42 | 49 | 52.7 | 3411 | 2 | Q98803 | Q98803 yellow feve |
| 43 | 49 | 52.7 | 3411 | 2 | Q6DV88 | Q6DV88 yellow feve |
| 44 | 49 | 52.7 | 3411 | 2 | Q6J3P1 | Q6J3P1 yellow feve |
| 45 | 49 | 52.7 | 3411 | 2 | Q6PX46 | Q6PX46 yellow feve |

ALIGNMENTS

RESULT 1
CP18 RABIT
ID CP18 RABIT STANDARD; PRT; 171 AA.
AC P25230;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Anticicrobial protein CAP18 precursor (18 kDa lipopolysaccharide-binding protein) (18 kDa cationic protein) (CAP18-A).
GN Name=CAP18;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_Taxid=9986;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 135-159.
RC TISSUE=Bone marrow;
RX MEDLINE=91354246; PubMed=1883348;
RA Larrick J.W., Morgan J.G., Palings I., Hirata M., Yen M.H.;
RT "Complementary DNA sequence of rabbit CAP18 -- a unique lipopolysaccharide binding protein.";
RT Biochem. Biophys. Res. Commun. 179:170-175(1991).
RN [2]
RP SEQUENCE OF 135-159, AND CHARACTERIZATION.
RX MEDLINE=94178952; PubMed=8132348;
RA Hirata M., Shimomura Y., Yoshida M., Morgan J.G., Palings I., Wilson D., Yen M.H., Wright S.C., Larrick J.W.;
RT "Characterization of a rabbit cationic protein (CAP18) with lipopolysaccharide-inhibitory activity.";
RT Infect. Immun. 62:1421-1426(1994).
RN [3]
RP SEQUENCE OF 135-154, AND CHARACTERIZATION.
RX MEDLINE=94075827; PubMed=8254193;
RA Larrick J.W., Hirata M., Zheng H., Zhong J., Bolin D., Cavallion J.-M., Warren H.S., Wright S.C.;
RT "A novel granulocyte-derived peptide with lipopolysaccharide-neutralizing activity.";
RT J. Immunol. 152:231-240(1994).
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=94148064; PubMed=8313956; DOI=10.1016/0014-5793(94)80395-1;
RA Tosai A., Scocchi M., Skerlavaj B., Gennaro R.;
RT "Identification and characterization of a primary antibacterial domain in CAP18, a lipopolysaccharide binding protein from rabbit leukocytes.";
RT FEBS Lett. 339:108-112(1994).
RN [5]
RP STRUCTURE BY NMR OF 135-166.
RX MEDLINE=95377455; PubMed=7649303; DOI=10.1016/0014-5793(95)00792-8;
RA Chen C., Brock R., Luh F., Chou P.-J., Larrick J.W., Huang R.-F., Huang T.-H.;
RT "The solution structure of the active domain of CAP18 -- a lipopolysaccharide binding protein from rabbit leukocytes.";
RT FEBS Lett. 370:46-52(1995).

GenCore version 5.1.6
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OM protein - protein search, using sw model:

Run on: May 2, 2005, 12:21:40 ; Search time 11.7821 Seconds

(without alignments)
155.160 Million cell updates/sec

Title: US-09-642-744d-22

Perfect score: 93
Sequence: 1 LRRFRNKIKELKKIGOKI 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 93 | 100.0 | 171 | 2 JQ1171 | 18K lipopolysaccha |
| 2 | 64 | 68.8 | 173 | 2 S70521 | cathelin-related p |
| 3 | 55 | 59.1 | 324 | 2 T07982 | probable choline-P |
| 4 | 55 | 59.1 | 326 | 2 T07983 | choline-phosphate |
| 5 | 52 | 55.9 | 329 | 2 T07981 | probable choline-P |
| 6 | 52 | 55.9 | 331 | 2 T07980 | probable choline-P |
| 7 | 49 | 52.7 | 142 | 2 E70356 | hypothetical prote |
| 8 | 49 | 52.7 | 332 | 2 H84730 | probable phosphol |
| 9 | 49 | 52.7 | 1163 | 1 GNMVY8 | genome polypeptid |
| 10 | 49 | 52.7 | 3411 | 1 GNMVY | genome polypeptid |
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| 12 | 48 | 51.6 | 152 | 2 C72227 | conserved hypotet |
| 13 | 48 | 51.6 | 293 | 2 T04851 | hypothetical prote |
| 14 | 48 | 51.6 | 497 | 2 E90061 | hypothetical prote |
| 15 | 47.5 | 51.1 | 274 | 2 C69444 | conserved hypotet |
| 16 | 47 | 50.5 | 174 | 2 F84426 | hypothetical prote |
| 17 | 47 | 50.5 | 259 | 2 G01485 | synthaxin - human |
| 18 | 47 | 50.5 | 288 | 2 J01615 | neuron-specific an |
| 19 | 47 | 50.5 | 298 | 2 A38141 | neutonal cell memb |
| 20 | 47 | 50.5 | 507 | 2 C82501 | conserved hypotet |
| 21 | 46 | 49.5 | 166 | 2 S41731 | antibacterial prot |
| 22 | 46 | 49.5 | 169 | 2 A82373 | polypeptide deform |
| 23 | 46 | 49.5 | 288 | 2 J00136 | synaptocanalin I - |
| 24 | 46 | 49.5 | 362 | 2 B48213 | synaxin 18 - rat |
| 25 | 46 | 49.5 | 362 | 2 T22204 | hypothetical prote |
| 26 | 46 | 49.5 | 519 | 2 T51496 | hypothetical prote |
| 27 | 46 | 49.5 | 1236 | 2 T18459 | hypothetical prote |
| 28 | 45 | 48.4 | 189 | 2 C64469 | hypothetical prote |
| 29 | 45 | 48.4 | 443 | 2 A82872 | ATP-dependent RNA |

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| 30 | 45 | 48.4 | 486 | 2 S74319 | RTG3 protein - yea |
| 31 | 45 | 48.4 | 522 | 2 A95059 | hypothetical prote |
| 32 | 45 | 48.4 | 522 | 2 H97927 | type I site-specif |
| 33 | 45 | 48.4 | 573 | 2 D90202 | methionyl-tRNA syn |
| 34 | 45 | 48.4 | 663 | 2 D97047 | DNA ligase (NAD de |
| 35 | 45 | 48.4 | 1631 | 1 SAZQK1 | major merozoit su |
| 36 | 45 | 48.4 | 1639 | 2 S05603 | probable major su |
| 37 | 45 | 48.4 | 1640 | 2 A24594 | conserved hypotet |
| 38 | 44.5 | 47.8 | 121 | 2 H70471 | hypothetical prote |
| 39 | 44.5 | 47.8 | 399 | 2 D86322 | hypothetical prote |
| 40 | 44 | 47.3 | 109 | 2 G64379 | hypothetical prote |
| 41 | 44 | 47.3 | 119 | 2 C90351 | hypothetical prote |
| 42 | 44 | 47.3 | 175 | 2 A64330 | hypothetical prote |
| 43 | 44 | 47.3 | 178 | 2 H97293 | hypoxanthine-guan |
| 44 | 44 | 47.3 | 188 | 2 E71157 | probable CDP-alcoh |
| 45 | 44 | 47.3 | 241 | 2 G86355 | hypothetical prote |

ALIGNMENTS

RESULT 1

JQ1171 18K lipopolysaccharide-binding protein precursor - rabbit

N/Alternate names: 18K cationic protein
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 06-Dec-1996

C/Accession: JQ1171, PS0226
R/Larrick, J.W.; Morgan, J.G.; Pallings, I.; Hirata, M.; Yen, M.H.

Biochem. Biophys. Res. Commun. 179, 170-175, 1991
A/Title: Complementary DNA sequence of rabbit CAP18-a unique lipopolysaccharide binding

A/Reference number: JQ1171, PMID:91554246; PMID:1883348
A/Accession: JQ1171

A/Molecule type: mRNA
A/Residues: 1171 <LAR>

A/Experimental source: bone marrow
A/Accession: PS0226

A/Molecule type: protein
A/Residues: 135-159, 'OIGOLL' <LA2>

A/Note: 157-Asp was also found
C/Superfamily: cathelin; cystatin homology

F/1-29/Domain: signal sequence #status predicted <SIG>
F/30-171/Product: 18K lipopolysaccharide-binding protein #status predicted <MAT>

Query Match Best Local Similarity 100.0%; Score 93; DB 2; Length 171;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRRFRNKIKELKKIGOKI 19
Db 140 LRRFRNKIKELKKIGOKI 158

RESULT 2

S70521 cathelin-related protein precursor - mouse

C/Species: Mus musculus (house mouse)
C/Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004

C/Accession: S70521
R/Popueva, A.E.; Zinovjeva, M.V.; Visser, J.W.M.; Zijlman, J.M.J.M.; Fibbe, W.E.; Bel

FEBS Lett. 391, 5-8, 1996
A/Title: A novel murine cathelin-like protein expressed in bone marrow.

A/Reference number: S70521, PMID:8706928
A/Accession: S70521

A/Status: preliminary
A/Molecule type: mRNA

A/Residues: 1-173 <POP>
A/Cross-references: UNIPROT:P51437, EMBL:X94353, NID:G1177533; P1DN:CAA64078.1; P1D:911

F/1-23/Domain: signal sequence #status predicted <SIG>
F/24-144/Domain: propeptide #status predicted <PRO>

F/145-173/Product: cathelin-related protein #status predicted <MAT>

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OM protein - protein search, using sw model

Run on: May 2, 2005, 13:03:56 ; Search time 51.6927 Seconds

(without alignments)
122.435 Million cell updates/sec

Title: US-09-642-744d-22

Perfect score: 93

Sequence: 1 LRKFRNKIKKKIKGQKI 19

BLOSUM62

Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 1426032 seqs, 333106140 residues

Total number of hits satisfying chosen parameters: 1426032

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA:*

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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

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4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

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16: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 93 | 100.0 | 32 | 14 | US-10-131-433-1 |
| 2 | 93 | 100.0 | 37 | 14 | US-10-060-102-5 |
| 3 | 93 | 100.0 | 37 | 15 | US-10-721-839-5 |
| 4 | 93 | 100.0 | 37 | 16 | US-10-344-709C-15 |
| 5 | 93 | 100.0 | 171 | 16 | US-10-344-709C-7 |
| 6 | 64 | 68.8 | 31 | 17 | US-10-399-442A-2 |
| 7 | 64 | 68.8 | 32 | 16 | US-10-344-709C-1 |
| 8 | 64 | 68.8 | 36 | 17 | US-10-470-048B-599 |
| 9 | 64 | 68.8 | 39 | 14 | US-10-060-102-1 |
| 10 | 64 | 68.8 | 39 | 15 | US-10-721-839-1 |
| 11 | 64 | 68.8 | 173 | 16 | US-10-344-709C-5 |
| 12 | 58 | 62.4 | 36 | 14 | US-10-268-171A-2 |
| 13 | 55 | 59.1 | 324 | 15 | US-10-389-566-1171 |

| | | | | | | |
|----|----|------|------|----|----------------------|--------------------|
| 14 | 55 | 59.1 | 326 | 14 | US-10-233-926-25 | Sequence 25, Appl |
| 15 | 55 | 59.1 | 326 | 15 | US-10-389-566-1172 | Sequence 1172, Ap |
| 16 | 54 | 58.1 | 39 | 14 | US-10-060-102-2 | Sequence 2, Appl1 |
| 17 | 54 | 58.1 | 39 | 15 | US-10-721-839-2 | Sequence 2, Appl1 |
| 18 | 52 | 55.9 | 329 | 14 | US-10-233-926-24 | Sequence 24, Appl1 |
| 19 | 52 | 55.9 | 329 | 15 | US-10-389-566-1173 | Sequence 1173, Ap |
| 20 | 52 | 55.9 | 331 | 14 | US-10-233-926-23 | Sequence 23, Appl |
| 21 | 52 | 55.9 | 331 | 15 | US-10-389-566-1174 | Sequence 1174, Ap |
| 22 | 52 | 55.9 | 1111 | 15 | US-10-382-122A-58098 | Sequence 58098, A |
| 23 | 52 | 55.9 | 1112 | 16 | US-10-398-186-22 | Sequence 1, Appl1 |
| 24 | 51 | 54.8 | 35 | 13 | US-10-205-150-1 | Sequence 22, Appl1 |
| 25 | 50 | 53.8 | 67 | 15 | US-10-424-599-250653 | Sequence 250653, |
| 26 | 49 | 52.7 | 51 | 15 | US-10-424-599-264915 | Sequence 264915, |
| 27 | 49 | 52.7 | 332 | 16 | US-10-389-566-1816 | Sequence 1816, Ap |
| 28 | 49 | 52.7 | 443 | 16 | US-10-767-701-44345 | Sequence 44345, A |
| 29 | 48 | 51.6 | 23 | 10 | US-09-820-053A-35 | Sequence 55, Appl |
| 30 | 48 | 51.6 | 23 | 14 | US-10-820-053A-35 | Sequence 34, Appl |
| 31 | 48 | 51.6 | 22 | 14 | US-10-109-171-55 | Sequence 2, Appl1 |
| 32 | 48 | 51.6 | 155 | 15 | US-10-336-603A-34 | Sequence 32, Appl |
| 33 | 48 | 51.6 | 178 | 13 | US-10-015-179-2 | Sequence 6, Appl1 |
| 34 | 48 | 51.6 | 178 | 15 | US-10-188-840-2 | Sequence 2, Appl1 |
| 35 | 48 | 51.6 | 338 | 15 | US-10-336-603A-32 | Sequence 32, Appl |
| 36 | 48 | 51.6 | 338 | 15 | US-10-155-435-6 | Sequence 6, Appl1 |
| 37 | 48 | 51.6 | 439 | 9 | US-09-815-242-5696 | Sequence 5696, Ap |
| 38 | 48 | 51.6 | 497 | 14 | US-10-358-917-14 | Sequence 14, Appl |
| 39 | 47 | 50.5 | 497 | 15 | US-10-282-122A-43955 | Sequence 43955, A |
| 40 | 47 | 50.5 | 60 | 16 | US-10-437-963-148381 | Sequence 148381, |
| 41 | 47 | 50.5 | 129 | 15 | US-10-424-599-264276 | Sequence 264276, |
| 42 | 47 | 50.5 | 194 | 14 | US-10-233-926-6 | Sequence 6, Appl1 |
| 43 | 47 | 50.5 | 259 | 16 | US-10-408-765A-807 | Sequence 807, App |
| 44 | 47 | 50.5 | 275 | 15 | US-10-424-599-216383 | Sequence 216383, |
| 45 | 47 | 50.5 | 288 | 10 | US-09-942-024-21 | Sequence 21, Appl |
| | | | | | US-09-942-024-23 | Sequence 23, Appl |

ALIGNMENTS

RESULT 1

US-10-131-433-1

Sequence 1, Application US/10131433

Publication No. US20030054422A1

GENERAL INFORMATION:

APPLICANT: UNILEVER, PLC

TITLE OF INVENTION: Lipopolysaccharide Immunoassay and Test Device

FILE REFERENCE: Lipopolysaccharide Immunoassay

CURRENT APPLICATION NUMBER: US/10/131,433

CURRENT FILING DATE: 2002-04-23

PRIOR APPLICATION NUMBER: US/09/545,180

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 8

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1

LENGTH: 32

TYPE: PRT

ORGANISM: Lactine

US-10-131-433-1

Query Match 100.0%; Score 93; DB 14; Length 32;

Best Local Similarity 100.0%; Pred. No. 8,4e-06;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRKFRNKIKKKIKGQKI 19

DB 6 LRKFRNKIKKKIKGQKI 24

RESULT 2

US-10-060-102-5

Sequence 5, Application US/10060102

Publication No. US20030028229A1

GENERAL INFORMATION:

APPLICANT: MAURY, WENDY

APPLICANT: STAPLETON, JACK

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 2, 2005, 12:18:40 ; Search time 18.0447 Seconds

(Without alignments)
78.601 Million cell updates/sec

Title: US-09-642-744d-22

Perfect score: 93

Sequence: 1 LKFRNKIKKIKIGOKI 19

Scoring table: BLOSUM62

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 3 | 87 | 93.5 | 29 | 1 | US-08-313-681A-7 |
| 4 | 87 | 93.5 | 29 | 3 | US-09-322-911-7 |
| 5 | 64 | 68.8 | 33 | 5 | PCT-US95-12080-4 |
| 6 | 55 | 59.1 | 16 | 1 | US-08-313-681A-11 |
| 7 | 55 | 59.1 | 16 | 3 | US-09-322-911-11 |
| 8 | 55 | 59.1 | 326 | 4 | US-09-735-846-25 |
| 9 | 52 | 55.9 | 329 | 4 | US-09-735-846-25 |
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| 11 | 49 | 52.7 | 331 | 4 | US-09-735-846-25 |
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| 14 | 47 | 50.5 | 190 | 4 | US-08-393-985-25 |
| 15 | 47 | 50.5 | 194 | 4 | US-09-735-846-6 |
| 16 | 47 | 50.5 | 259 | 4 | US-09-509-738C-25 |
| 17 | 47 | 50.5 | 285 | 1 | US-08-393-985-23 |
| 18 | 47 | 50.5 | 288 | 1 | US-08-393-985-2 |
| 19 | 47 | 50.5 | 288 | 3 | US-08-558-135-4 |
| 20 | 47 | 50.5 | 306 | 3 | US-08-819-286-3 |
| 21 | 47 | 50.5 | 306 | 3 | US-09-134-001C-4678 |
| 22 | 46 | 49.5 | 27 | 1 | US-09-735-846-20 |
| 23 | 46 | 49.5 | 27 | 1 | US-08-231-730A-15 |
| 24 | 46 | 49.5 | 27 | 1 | US-08-427-001C-15 |
| 25 | 46 | 49.5 | 27 | 1 | US-08-457-798-15 |
| 26 | 46 | 49.5 | 27 | 1 | US-08-457-798-15 |
| 27 | 46 | 49.5 | 27 | 1 | US-08-457-798-15 |
| 28 | 46 | 49.5 | 27 | 2 | US-08-505-486-15 |

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| 28 | 46 | 49.5 | 27 | 2 | US-08-505-486-62 | Sequence 62, Appl |
| 29 | 46 | 49.5 | 27 | 3 | US-08-689-489C-15 | Sequence 15, Appl |
| 30 | 46 | 49.5 | 27 | 3 | US-08-801-028-15 | Sequence 15, Appl |
| 31 | 46 | 49.5 | 27 | 3 | US-08-801-028-62 | Sequence 62, Appl |
| 32 | 46 | 49.5 | 27 | 3 | US-09-340-154-15 | Sequence 15, Appl |
| 33 | 46 | 49.5 | 27 | 3 | US-09-340-154-62 | Sequence 62, Appl |
| 34 | 46 | 49.5 | 27 | 3 | US-09-232-802A-15 | Sequence 15, Appl |
| 35 | 46 | 49.5 | 27 | 4 | US-09-482-611B-15 | Sequence 15, Appl |
| 36 | 46 | 49.5 | 27 | 4 | US-09-482-611B-62 | Sequence 62, Appl |
| 37 | 46 | 49.5 | 27 | 5 | US-09-019-922A-15 | Sequence 15, Appl |
| 38 | 46 | 49.5 | 27 | 5 | PCT-US94-06176-15 | Sequence 15, Appl |
| 39 | 46 | 49.5 | 27 | 5 | PCT-US94-06176-15 | Sequence 15, Appl |
| 40 | 46 | 49.5 | 27 | 5 | PCT-US95-04335-15 | Sequence 15, Appl |
| 41 | 46 | 49.5 | 27 | 5 | PCT-US95-04718-15 | Sequence 15, Appl |
| 42 | 46 | 49.5 | 27 | 5 | PCT-US95-09338-15 | Sequence 15, Appl |
| 43 | 46 | 49.5 | 27 | 5 | PCT-US95-09338-62 | Sequence 62, Appl |
| 44 | 46 | 49.5 | 27 | 5 | PCT-US95-09339-15 | Sequence 15, Appl |
| 45 | 46 | 49.5 | 27 | 5 | PCT-US95-09339-62 | Sequence 62, Appl |

ALIGNMENTS

RESULT 1
US-08-313-681A-4
Sequence 4, Application US/08313681A
Patent No. 5618675
GENERAL INFORMATION:
APPLICANT: Larick, James W.
APPLICANT: Wright, Susan C.
APPLICANT: Hiraata, Mishima
TITLE OF INVENTION: Human Cationic Proteins Having
TITLE OF INVENTION: Lipopolysaccharide Binding and Anti-Coagulant Activity
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,681A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15325-9-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 171 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-313-681A-4
Query Match 100.0%; Score 93; DB 1; Length 171;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1 LKFRNKIKKIKIGOKI 19
140 LKFRNKIKKIKIGOKI 158

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:17:55 ; Search time 66.6061 Seconds

(without alignment)
110.327 Million cell updates/sec

Title: US-09-642-744D-22

Perfect score: 93

Sequence: 1 LRRFRNKKIKKKIKGKI 19

Scoring table: BLAST62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp19808:*
2: geneseqp19908:*
3: geneseqp20008:*
4: geneseqp20018:*
5: geneseqp20028:*
6: geneseqp20038:*
7: geneseqp20048:*
8: geneseqp20058:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|------------|--------------------|
| 1 | 93 | 100.0 | 19 | 4 AAB70669 | Abb70669 Lupine RC |
| 2 | 93 | 100.0 | 21 | 4 AAB70670 | Abb70670 Lupine RC |
| 3 | 93 | 100.0 | 22 | 4 AAB70668 | Abb70668 Lupine RC |
| 4 | 93 | 100.0 | 24 | 6 AAE34416 | Aae34416 Rabbit RC |
| 5 | 93 | 100.0 | 24 | 8 ADK70763 | Adk70763 Rabbit CA |
| 6 | 93 | 100.0 | 26 | 6 AAE34418 | Aae34418 Rabbit CA |
| 7 | 93 | 100.0 | 26 | 6 AAE34417 | Aae34417 Rabbit CA |
| 8 | 93 | 100.0 | 26 | 6 AAE34419 | Aae34419 Rabbit CA |
| 9 | 93 | 100.0 | 26 | 6 AAE34421 | Aae34421 Rabbit CA |
| 10 | 93 | 100.0 | 26 | 6 AAE34420 | Aae34420 Rabbit CA |
| 11 | 93 | 100.0 | 26 | 8 ADK70762 | Adk70762 Rabbit CA |
| 12 | 93 | 100.0 | 32 | 3 AAB28486 | Aab28486 Rabbit II |
| 13 | 93 | 100.0 | 32 | 8 ADK70761 | Adk70761 Rabbit CA |
| 14 | 93 | 100.0 | 37 | 4 AAB70665 | Abb70665 Lupine RC |
| 15 | 93 | 100.0 | 37 | 5 ABB07711 | Abb07711 Antimicro |
| 16 | 93 | 100.0 | 37 | 5 ABP53272 | Abp53272 Sheep nat |
| 17 | 93 | 100.0 | 38 | 4 AAB51193 | Aab51193 E. coli A |
| 18 | 93 | 100.0 | 142 | 8 ABB07706 | Abb07706 Rabbit CA |
| 19 | 93 | 100.0 | 171 | 5 ABB07703 | Abb07703 Rabbit pe |
| 20 | 89 | 95.7 | 24 | 8 ADK70764 | Adk70764 Rabbit CA |
| 21 | 87 | 93.5 | 29 | 3 AAB45671 | Aa45671 N terminu |
| 22 | 87 | 93.5 | 29 | 3 AAB07903 | Abb07903 Putative |
| 23 | 79 | 84.9 | 18 | 4 AAB70667 | Abb70667 Lupine RC |
| 24 | 79 | 84.9 | 21 | 4 AAB70666 | Abb70666 Lupine RC |
| 25 | 75 | 80.6 | 15 | 4 AAB70671 | Abb70671 Lupine RC |

| | | | | | |
|----|----|------|-----|------------|--------------------|
| 26 | 73 | 78.5 | 20 | 8 ADK70765 | Adk70765 Rabbit CA |
| 27 | 64 | 68.8 | 31 | 5 AAO15559 | Aao15559 Murine ca |
| 28 | 64 | 68.8 | 32 | 5 ABB07697 | Abb07697 Murine ca |
| 29 | 64 | 68.8 | 33 | 2 AAB94449 | Aab94449 Mouse ant |
| 30 | 64 | 68.8 | 39 | 5 ABP53268 | Abp53268 Mouse nat |
| 31 | 64 | 68.8 | 173 | 5 ABB07701 | Abb07701 Murine ca |
| 32 | 62 | 66.7 | 15 | 4 AAB70672 | Abb70672 Lupine RC |
| 33 | 62 | 66.7 | 17 | 4 AAB70673 | Abb70673 Lupine RC |
| 34 | 58 | 62.4 | 36 | 4 AAG66421 | Aag66421 Mouse cat |
| 35 | 58 | 62.4 | 36 | 5 AAU09819 | Aau09819 Mouse cat |
| 36 | 58 | 62.4 | 36 | 5 ABG31966 | Abg31966 Mouse cat |
| 37 | 58 | 62.4 | 36 | 5 ABB31663 | Abb31663 Mouse cat |
| 38 | 58 | 62.4 | 36 | 5 AAU76940 | Aau76940 Mouse cat |
| 39 | 58 | 62.4 | 36 | 6 ABP58358 | Abp58358 Mouse cat |
| 40 | 58 | 62.4 | 36 | 8 ADJ51139 | Adj51139 Murine ca |
| 41 | 55 | 59.1 | 16 | 2 AAR45673 | Aar45673 RNP hepa |
| 42 | 55 | 59.1 | 16 | 3 AAB07905 | Abb07905 Heparin-B |
| 43 | 55 | 59.1 | 324 | 8 ADJ49167 | Adj49167 O11-aseoc |
| 44 | 55 | 59.1 | 326 | 6 ADA06238 | Ada06238 Rape chol |
| 45 | 55 | 59.1 | 326 | 8 ADJ49168 | Adj49168 O11-aseoc |

ALIGNMENTS

RESULT 1

AAB70669 standard; peptide; 19 AA.

ID AAB70669 (first entry)

DE Lupine RCAP 18 cathelicidin derived antimicrobial peptide SEQ ID NO:22.

XX Ovine; SMAP29; lupine; RCAP 18; cathelicidin; antimicrobial;
XX bactericidal; antibiotic; antiviral; microbial growth inhibitor;
XX proliferation inhibitor; gene therapy; Pseudomonas aeruginosa;
XX Burkholderia cepacia; Alcaligenes; Xanthomonas.

OS Oryzocolagus cuniculus.

XX WO200112668-A1.

XX 22-FEB-2001.

XX 18-AUG-2000; 2000WO-US022781.

XX 18-AUG-1999; 99US-0149886P.

XX (IOWA) UNIV IOWA RES FOUND.

XX (REGC) UNIV CALIFORNIA.

XX Tack BE, Mccray P, Welsh M, Travis SM, Lehrer R;

XX WPI; 2001-234911/24.

XX New antimicrobial peptides useful as antibiotics for inhibiting growth
XX and proliferation of microbes, and for treating microbial infections.

XX Claim 1; Page 103; 137pp; English.

XX AAB70648 to AAB70675 represent antimicrobial peptides (I) of which
XX AAB70648 to AAB70664, AAB70674 and AAB70675 are derived from the ovine
XX SMAP 29 cathelicidin family peptide, and AAB70673 are derived
XX from the lupine RCAP 18 cathelicidin family peptide. (I) have antibiotic,
XX antimicrobial and antiviral activities, and can be used as microbial
XX growth and proliferation inhibitors and in gene therapy. (II) are useful
XX for inhibiting microbial growth in an environment capable of sustaining
XX such growth, for inhibiting microbial growth or strain in a host, and
XX inhibiting the growth of drug-resistant microbial strains such as
XX Pseudomonas aeruginosa, Burkholderia cepacia, Alcaligenes and Xanthomonas

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:17:06 ; Search time 68.6425 Seconds

(without alignments)
164,122 Million cell updates/sec

Title: US-09-642-744D-21

Sequence: 108

Sequence: 1 RKRLRKFRANKIKKXKIGCKI 22

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: uniprot_sprotc:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 108 | 100.0 | 171 | 1 | CP18 RABIT |
| 2 | 64 | 59.3 | 173 | 1 | GRAM MOUSE |
| 3 | 61 | 56.5 | 511 | 2 | Q7P8I9 |
| 4 | 60 | 55.6 | 324 | 2 | Q42621 |
| 5 | 60 | 55.6 | 326 | 2 | Q42622 |
| 6 | 58 | 53.7 | 170 | 2 | Q9GLV5 |
| 7 | 57 | 52.8 | 171 | 2 | Q71KMS |
| 8 | 57 | 52.8 | 329 | 2 | Q42620 |
| 9 | 57 | 52.8 | 331 | 2 | Q42619 |
| 10 | 54 | 50.0 | 331 | 2 | Q42555 |
| 11 | 54 | 50.0 | 332 | 2 | Q92V56 |
| 12 | 54 | 50.0 | 400 | 2 | Q89295 |
| 13 | 54 | 50.0 | 400 | 2 | Q89297 |
| 14 | 54 | 50.0 | 400 | 2 | Q89299 |
| 15 | 54 | 50.0 | 400 | 2 | Q89304 |
| 16 | 54 | 50.0 | 400 | 2 | Q89311 |
| 17 | 54 | 50.0 | 400 | 2 | Q89317 |
| 18 | 54 | 50.0 | 508 | 1 | YJ13 FUSNN |
| 19 | 54 | 50.0 | 778 | 2 | P89915 |
| 20 | 54 | 50.0 | 778 | 2 | Q77X62 |
| 21 | 54 | 50.0 | 778 | 2 | Q77X64 |
| 22 | 54 | 50.0 | 778 | 2 | Q9W9B8 |
| 23 | 54 | 50.0 | 3411 | 1 | POLG_YEFV1 |
| 24 | 54 | 50.0 | 3411 | 1 | POLG_YEFV2 |
| 25 | 54 | 50.0 | 3411 | 1 | O91857 |
| 26 | 54 | 50.0 | 3411 | 2 | O98803 |
| 27 | 54 | 50.0 | 3411 | 2 | O6DV88 |
| 28 | 54 | 50.0 | 3411 | 2 | O6J3P1 |
| 29 | 54 | 50.0 | 3411 | 2 | O6PX46 |
| 30 | 54 | 50.0 | 3411 | 2 | O89275 |
| 31 | 54 | 50.0 | 3411 | 2 | O89276 |

ALIGNMENTS

| | | | | | | |
|----|----|------|------|---|------------|---------------------|
| 32 | 54 | 50.0 | 3411 | 2 | O89277 | O89277 yellow feve |
| 33 | 54 | 50.0 | 3411 | 2 | O89278 | O89278 yellow feve |
| 34 | 54 | 50.0 | 3411 | 2 | O9YRV3 | O9YRV3 yellow feve |
| 35 | 54 | 50.0 | 3411 | 2 | O9YVNO | O9YVNO yellow feve |
| 36 | 54 | 50.0 | 3411 | 2 | O9YVNI | O9YVNI yellow feve |
| 37 | 54 | 50.0 | 3411 | 2 | O9YVNZ | O9YVNZ yellow feve |
| 38 | 53 | 49.1 | 178 | 2 | O60831 | O60831 homo sapien |
| 39 | 53 | 49.1 | 178 | 2 | O9JIG8 | O9JIG8 m dxtmx39e |
| 40 | 53 | 49.1 | 400 | 2 | O89315 | O89315 yellow feve |
| 41 | 53 | 49.1 | 809 | 2 | O6FTT3 | O6FTT3 candida gla |
| 42 | 53 | 49.1 | 1163 | 1 | POLG_YEFV8 | P29165 yellow feve |
| 43 | 53 | 49.1 | 3787 | 2 | O81126 | O81126 plasmodium |
| 44 | 52 | 48.1 | 123 | 2 | O9NH16 | O9NH16 plasmodium |
| 45 | 52 | 48.1 | 228 | 2 | O74MC7 | O74MC7 nanosarchaeu |

RESULT 1
CP18 RABIT
ID CP18 RABIT STANDARD; PRT; 171 AA.
AC P25230;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Antimicrobial protein CAP18 precursor (18 kDa lipopolysaccharide-binding protein) (18 kDa cationic protein) (CAP18-A).
GN Name=CAP18;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_Taxid=9986;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 135-159.
RC TISSUE=Bone marrow; PubMed=1883348;
RX MEDLINE=91354246; PubMed=1883348;
RA Larrick J.W., Morgan J.G., Palings I., Hirata M., Yen M.H.;
RT "Complementary DNA sequence of rabbit CAP18 -- a unique
RT lipopolysaccharide binding protein.";
RL Biochem. Biophys. Res. Commun. 179:170-175(1991).
RN [2]
RP SEQUENCE OF 135-159, AND CHARACTERIZATION.
RX MEDLINE=94178952; PubMed=812348;
RA Hirata M., Shimomura Y., Yoshida M., Morgan J.G., Palings I.,
RA Wilson D., Yen M.H., Wright S.C., Larrick J.W.;
RT "Characterization of a rabbit cationic protein (CAP18) with
RT lipopolysaccharide-inhibitory activity.";
RL Infect. Immun. 62:1421-1426(1994).
RN [3]
RP SEQUENCE OF 135-154, AND CHARACTERIZATION.
RX MEDLINE=94075827; PubMed=8254193;
RA Larrick J.W., Hirata M., Zheng H., Zhong J., Bolin D.,
RA Cavallion J.-M., Warren H.S., Wright S.C.;
RT "A novel granulocyte-derived peptide with lipopolysaccharide-
RT neutralizing activity.";
RL J. Immunol. 152:231-240(1994).
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=94148064; PubMed=8313956; DOI=10.1016/0014-5793(94)80395-1;
RA Tossi A., Scocchi M., Serravallo B., Gennaro R.;
RT "Identification and characterization of a primary antibacterial domain
RT in CAP18, a lipopolysaccharide binding protein from rabbit
RT leukocytes.";
RL FEBS Lett. 339:108-112(1994).
RN [5]
RP STRUCTURE BY NMR OF 135-166.
RX MEDLINE=95377455; PubMed=7649303; DOI=10.1016/0014-5793(95)00792-8;
RA Chen C., Brock R., Luh F., Chou P.-J., Larrick J.W., Huang R.-F.,
RA Huang T.-H.;
RT "The solution structure of the active domain of CAP18 -- a
RT lipopolysaccharide binding protein from rabbit leukocytes.";
RL FEBS Lett. 370:46-52(1995).

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OM protein - protein search, using SW model

Run on: May 2, 2005, 12:21:40 / Search time 13.6425 Seconds

(without alignments)
155.160 Million cell updates/sec

Title: US-09-642-744D-21

Perfect score: 108

Sequence: 1 RKRLKFRNKIKKKIKGKI 22

Scoring table:

BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|---|
| 1 | 108 | 100.0 | 171 | 2 JQ1171 | 18K lipopolysaccharide-binding protein precursor - rabbit |
| 2 | 64 | 59.3 | 173 | 2 S70521 | cathelin-related protein |
| 3 | 60 | 55.6 | 324 | 2 T07982 | probable choline-P |
| 4 | 60 | 55.6 | 326 | 2 T07983 | choline-phosphate |
| 5 | 57 | 52.8 | 329 | 2 T07981 | probable choline-P |
| 6 | 57 | 52.8 | 331 | 2 T07980 | probable phospholipase |
| 7 | 54 | 50.0 | 332 | 2 H84730 | probable phospholipase |
| 8 | 54 | 50.0 | 3411 | 1 GNMVY | genome polypeptide |
| 9 | 54 | 50.0 | 3411 | 1 GNMVY | genome polypeptide |
| 10 | 53 | 49.1 | 1163 | 1 GNMVY | genome polypeptide |
| 11 | 51 | 47.2 | 166 | 2 S41731 | genome polypeptide |
| 12 | 51 | 47.2 | 241 | 2 G86355 | antibacterial protein |
| 13 | 50 | 46.3 | 73 | 2 T03182 | hypothetical protein |
| 14 | 50 | 46.3 | 831 | 2 S44843 | hypothetical protein |
| 15 | 49.5 | 45.8 | 121 | 2 H70471 | hypothetical protein |
| 16 | 49.5 | 45.8 | 121 | 2 H70471 | hypothetical protein |
| 17 | 49.5 | 45.8 | 121 | 2 H70471 | hypothetical protein |
| 18 | 49.5 | 45.8 | 121 | 2 H70471 | hypothetical protein |
| 19 | 48.5 | 44.9 | 354 | 2 B70356 | DNA repair and recombination |
| 20 | 48.5 | 44.9 | 354 | 2 B70356 | DNA repair and recombination |
| 21 | 48.5 | 44.9 | 354 | 2 B70356 | DNA repair and recombination |
| 22 | 48.5 | 44.9 | 354 | 2 B70356 | DNA repair and recombination |
| 23 | 48.5 | 44.9 | 354 | 2 B70356 | DNA repair and recombination |
| 24 | 48.5 | 44.9 | 354 | 2 B70356 | DNA repair and recombination |
| 25 | 48.5 | 44.9 | 354 | 2 B70356 | DNA repair and recombination |
| 26 | 48.5 | 44.9 | 354 | 2 B70356 | DNA repair and recombination |
| 27 | 48.5 | 44.9 | 354 | 2 B70356 | DNA repair and recombination |
| 28 | 48.5 | 44.9 | 354 | 2 B70356 | DNA repair and recombination |
| 29 | 48.5 | 44.9 | 354 | 2 B70356 | DNA repair and recombination |

| | | | | | |
|----|----|------|-----|----------|-------------------------|
| 30 | 47 | 43.5 | 94 | 2 T43076 | hypothetical protein |
| 31 | 47 | 43.5 | 153 | 2 JN0344 | myoglobin - Balkan |
| 32 | 47 | 43.5 | 167 | 2 S68967 | antibacterial peptide |
| 33 | 47 | 43.5 | 174 | 2 F84426 | hypothetical protein |
| 34 | 47 | 43.5 | 259 | 2 S57283 | 14-3-3 brain protein |
| 35 | 47 | 43.5 | 259 | 2 S57283 | 14-3-3 brain protein |
| 36 | 47 | 43.5 | 288 | 2 JN0466 | epitaxin - human |
| 37 | 47 | 43.5 | 288 | 2 JN0466 | epitaxin - human |
| 38 | 47 | 43.5 | 298 | 2 A38141 | neuron-specific antigen |
| 39 | 47 | 43.5 | 305 | 2 T23929 | neuron-specific antigen |
| 40 | 47 | 43.5 | 655 | 2 S57119 | hypothetical protein |
| 41 | 47 | 43.5 | 655 | 2 S57119 | hypothetical protein |
| 42 | 47 | 43.5 | 788 | 2 T50203 | hypothetical protein |
| 43 | 47 | 43.5 | 822 | 2 S77188 | yeast RNAase P/MRP |
| 44 | 47 | 43.5 | 822 | 2 S77188 | DNA mismatch repair |
| 45 | 46 | 42.6 | 162 | 2 H70314 | hypothetical protein |
| | | | 169 | 2 A82373 | polypeptide domain |

ALIGNMENTS

RESULT 1

JQ1171

18K lipopolysaccharide-binding protein precursor - rabbit

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #ext_change 06-Dec-1996

C/Accession: JQ1171; P80226

A/Accession: JQ1171

A/Molecule type: mRNA

A/Residues: 1-171 <LA>

A/Experimental source: bone marrow

A/Accession: P80226

A/Molecule type: protein

A/Residues: 135-159, 'QIGQL' <LA2>

A/Note: 157-Asp was also found

C/Superfamily: cathelin; cystatin homology

F.1-29/Domains: signal sequence #status predicted <SIG>

F.30-171/Product: 18K lipopolysaccharide-binding protein #status predicted <MAT>

Query Match

Best Local Similarity 100.0%; Score 108; DB 2; Length 171;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 137 RKRLKFRNKIKKKIKGKI 158

QY 1 RKRLKFRNKIKKKIKGKI 22

DB 137 RKRLKFRNKIKKKIKGKI 158

RESULT 2

S70521

cathelin-related protein precursor - mouse

C/Species: Mus musculus (house mouse)

C/Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #ext_change 09-Jul-2004

C/Accession: S70521

A/Accession: S70521

A/Molecule type: preliminary

A/Residues: 1-173 <POP>

A/Cross-reference: UNIPROT:P51437; EMBL:X94353; NID:G1177533; PIDD:CAA64078.1; PIDD:G11

C/Superfamily: cathelin; cystatin homology

F.1-23/Domains: signal sequence #status predicted <SIG>

F.24-144/Domains: propeptide #status predicted <PRO>

F.145-173/Product: cathelin-related protein #status predicted <MAT>

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OM protein - protein search, using ew model

Run on: May 2, 2005, 13:03:56 ; Search time 59.8548 Seconds

(without alignment)
122.435 Million cell updates/sec

Title: US-09-642-744d-21

Sequence: 1 RKRLRRFRNKIKKIKIGOKI 22

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 1426032 seqs, 333106140 residues

Total number of hits satisfying chosen parameters: 1426032

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Listed first 45 summaries

Published Applications AA:*

1: /cgn2_6/ptodata/1/pubppa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubppa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubppa/US06_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubppa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubppa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubppa/PCTUS_PUBCOMB.pep:*

7: /cgn2_6/ptodata/1/pubppa/US08_NEW_PUB.pep:*

8: /cgn2_6/ptodata/1/pubppa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubppa/US09B_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubppa/US09C_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubppa/US09_NEW_PUB.pep:*

13: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubppa/US10B_PUBCOMB.pep:*

15: /cgn2_6/ptodata/1/pubppa/US10C_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep:*

17: /cgn2_6/ptodata/1/pubppa/US10_NEW_PUB.pep:*

18: /cgn2_6/ptodata/1/pubppa/US10_NEW_PUB.pep:*

19: /cgn2_6/ptodata/1/pubppa/US60_NEW_PUB.pep:*

20: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 108 | 100.0 | 32 | 14 | US-10-131-433-1 |
| 2 | 108 | 100.0 | 37 | 14 | US-10-060-102-5 |
| 3 | 108 | 100.0 | 37 | 15 | US-10-721-839-5 |
| 4 | 108 | 100.0 | 37 | 16 | US-10-344-709C-15 |
| 5 | 108 | 100.0 | 171 | 16 | US-10-344-709C-7 |
| 6 | 59.3 | 59.3 | 31 | 17 | US-10-399-442A-2 |
| 7 | 64 | 59.3 | 32 | 16 | US-10-344-709C-1 |
| 8 | 64 | 59.3 | 36 | 17 | US-10-470-048B-599 |
| 9 | 64 | 59.3 | 39 | 14 | US-10-060-102-1 |
| 10 | 64 | 59.3 | 39 | 15 | US-10-721-839-1 |
| 11 | 64 | 59.3 | 173 | 16 | US-10-344-709C-5 |
| 12 | 60 | 55.6 | 324 | 15 | US-10-389-566-1171 |
| 13 | 60 | 55.6 | 326 | 14 | US-10-233-926-25 |

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|----|------|------|------|----|----------------------|--------------------|
| 14 | 60 | 55.6 | 326 | 15 | US-10-389-566-1172 | Sequence 1172, Ap |
| 15 | 58 | 53.7 | 36 | 14 | US-10-269-171A-2 | Sequence 2, Appli |
| 16 | 57 | 52.8 | 329 | 14 | US-10-233-926-24 | Sequence 24, Appli |
| 17 | 57 | 52.8 | 329 | 15 | US-10-389-566-1173 | Sequence 1173, Ap |
| 18 | 57 | 52.8 | 331 | 14 | US-10-233-926-23 | Sequence 23, Appli |
| 19 | 57 | 52.8 | 331 | 15 | US-10-389-566-1174 | Sequence 1174, Ap |
| 20 | 56 | 51.9 | 51 | 15 | US-10-424-599-264915 | Sequence 264915, |
| 21 | 54 | 50.0 | 39 | 14 | US-10-060-102-2 | Sequence 2, Appli |
| 22 | 54 | 50.0 | 39 | 15 | US-10-721-839-2 | Sequence 2, Appli |
| 23 | 54 | 50.0 | 194 | 14 | US-10-233-926-6 | Sequence 6, Appli |
| 24 | 54 | 50.0 | 318 | 15 | US-10-389-566-673 | Sequence 673, App |
| 25 | 54 | 50.0 | 318 | 15 | US-10-389-566-674 | Sequence 674, App |
| 26 | 54 | 50.0 | 332 | 15 | US-10-389-566-1816 | Sequence 1816, Ap |
| 27 | 54 | 50.0 | 363 | 14 | US-10-233-926-20 | Sequence 20, Appli |
| 28 | 53 | 49.1 | 155 | 15 | US-10-336-603A-34 | Sequence 34, Appli |
| 29 | 53 | 49.1 | 178 | 13 | US-10-015-179-2 | Sequence 2, Appli |
| 30 | 53 | 49.1 | 178 | 15 | US-10-188-840-2 | Sequence 2, Appli |
| 31 | 53 | 49.1 | 178 | 15 | US-10-336-603A-32 | Sequence 32, Appli |
| 32 | 53 | 49.1 | 641 | 16 | US-10-437-963-181519 | Sequence 181519, |
| 33 | 52 | 48.1 | 1111 | 15 | US-10-282-122A-58098 | Sequence 58098, A |
| 34 | 52 | 48.1 | 1112 | 16 | US-10-398-186-22 | Sequence 181519, |
| 35 | 51 | 47.2 | 23 | 10 | US-09-820-053A-55 | Sequence 22, Appli |
| 36 | 51 | 47.2 | 23 | 14 | US-10-109-171-55 | Sequence 55, Appli |
| 37 | 51 | 47.2 | 35 | 13 | US-10-205-150-1 | Sequence 243585, |
| 38 | 50 | 46.3 | 59 | 15 | US-10-424-599-243585 | Sequence 250653, |
| 39 | 50 | 46.3 | 67 | 15 | US-10-424-599-250653 | Sequence 148301, |
| 40 | 50 | 46.3 | 83 | 16 | US-10-437-963-148201 | Sequence 116556, |
| 41 | 50 | 46.3 | 257 | 16 | US-10-437-963-116556 | Sequence 116556, |
| 42 | 50 | 46.3 | 258 | 9 | US-09-828-447-13 | Sequence 13, Appli |
| 43 | 50 | 46.3 | 1176 | 14 | US-10-032-585-7782 | Sequence 7782, Ap |
| 44 | 49.5 | 45.8 | 112 | 16 | US-10-767-701-35738 | Sequence 35738, A |
| 45 | 49.5 | 45.4 | 123 | 9 | US-09-820-893-81 | Sequence 81, Appli |

ALIGNMENTS

RESULT 1

US-10-131-433-1

Sequence 1, Application US/10131433

Publication No. US20030054422A1

GENERAL INFORMATION:

APPLICANT: UNILEVER, PLC

TITLE OF INVENTION: Lipopolysaccharide Immunoassay and Test Device

FILE REFERENCE: Lipopolysaccharide Immunoassay

CURRENT APPLICATION NUMBER: US/10/131,433

CURRENT FILING DATE: 2002-04-23

PRIOR APPLICATION NUMBER: US/09/545,180

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 8

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1

LENGTH: 32

TYPE: PRT

ORGANISM: Lاپine

US-10-131-433-1

Query Match

Best Local Similarity 100.0%; Score 108; DB 14;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RKRLRRFRNKIKKIKIGOKI 22

Db 3 RKRLRRFRNKIKKIKIGOKI 24

RESULT 2

US-10-060-102-5

Sequence 5, Application US/10060102

Publication No. US20030022829A1

GENERAL INFORMATION:

APPLICANT: MAURY, WENDY

APPLICANT: STAPLETON, JACK

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:18:40 ; Search time 20.8939 Seconds

(Without alignments)
78.601 Million cell updates/sec

Title: US-09-642-744D-21

Sequence: 1 RKRLKFRNKIKKXIGKI 22

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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5: /cgn2_6/prodata/1/iaa/PCUS_COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfilest1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 108 | 100.0 | 171 | 1 | US-08-313-681A-4 |
| 2 | 108 | 100.0 | 171 | 3 | US-09-322-911-4 |
| 3 | 102 | 94.4 | 29 | 1 | US-08-313-681A-7 |
| 4 | 102 | 94.4 | 29 | 3 | US-09-322-911-7 |
| 5 | 70 | 64.8 | 16 | 1 | US-08-313-681A-11 |
| 6 | 70 | 64.8 | 16 | 3 | US-09-322-911-11 |
| 7 | 64 | 59.3 | 33 | 5 | PCT-US95-12080-4 |
| 8 | 60 | 55.6 | 326 | 4 | US-09-735-846-25 |
| 9 | 57 | 52.8 | 329 | 4 | US-09-735-846-24 |
| 10 | 54 | 50.0 | 194 | 4 | US-09-735-846-23 |
| 11 | 54 | 50.0 | 194 | 4 | US-09-735-846-6 |
| 12 | 54 | 50.0 | 363 | 4 | US-09-735-846-20 |
| 13 | 54 | 50.0 | 363 | 4 | US-09-735-846-20 |
| 14 | 53 | 49.1 | 37 | 1 | US-09-452-618-53 |
| 15 | 53 | 49.1 | 37 | 3 | US-08-313-681A-6 |
| 16 | 50 | 46.3 | 258 | 3 | US-09-322-911-6 |
| 17 | 50 | 46.3 | 258 | 4 | US-09-828-447-13 |
| 18 | 49 | 45.4 | 18 | 4 | US-09-248-796A-18727 |
| 19 | 49 | 45.4 | 123 | 4 | US-09-525-262A-10 |
| 20 | 49 | 45.4 | 123 | 4 | US-09-148-545-187 |
| 21 | 49 | 45.4 | 123 | 4 | US-09-148-545-243 |
| 22 | 49 | 45.4 | 452 | 4 | US-09-695-795A-6 |
| 23 | 48 | 44.4 | 223 | 4 | US-09-889-738-21 |
| 24 | 48 | 44.4 | 223 | 4 | US-09-344-62A-12 |
| 25 | 48 | 44.4 | 269 | 4 | US-09-744-989C-3 |
| 26 | 48 | 44.4 | 287 | 4 | US-09-744-989C-1 |
| 27 | 48 | 44.4 | 287 | 4 | US-09-744-989C-5 |
| | | | 1244 | 4 | US-09-949-016-11702 |

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|----|----|------|-----|---|-------------------|-------------------|
| 28 | 47 | 43.5 | 103 | 3 | US-09-308-388-1 | Sequence 1, Appl |
| 29 | 47 | 43.5 | 187 | 3 | US-08-493-071-16 | Sequence 16, Appl |
| 30 | 47 | 43.5 | 190 | 3 | US-08-393-985-25 | Sequence 25, Appl |
| 31 | 47 | 43.5 | 236 | 3 | US-08-493-071-15 | Sequence 15, Appl |
| 32 | 47 | 43.5 | 259 | 4 | US-09-509-738C-25 | Sequence 25, Appl |
| 33 | 47 | 43.5 | 263 | 4 | US-08-393-985-23 | Sequence 23, Appl |
| 34 | 47 | 43.5 | 277 | 1 | US-08-690-457-5 | Sequence 5, Appl |
| 35 | 47 | 43.5 | 277 | 2 | US-08-628-187-5 | Sequence 5, Appl |
| 36 | 47 | 43.5 | 277 | 3 | US-08-493-071-3 | Sequence 3, Appl |
| 37 | 47 | 43.5 | 285 | 1 | US-08-393-985-2 | Sequence 2, Appl |
| 38 | 47 | 43.5 | 287 | 1 | US-08-690-457-4 | Sequence 4, Appl |
| 39 | 47 | 43.5 | 287 | 2 | US-08-628-187-4 | Sequence 2, Appl |
| 40 | 47 | 43.5 | 287 | 3 | US-08-493-071-2 | Sequence 2, Appl |
| 41 | 47 | 43.5 | 288 | 1 | US-08-337-602-4 | Sequence 4, Appl |
| 42 | 47 | 43.5 | 288 | 1 | US-08-690-457-3 | Sequence 3, Appl |
| 43 | 47 | 43.5 | 288 | 2 | US-08-628-187-3 | Sequence 3, Appl |
| 44 | 47 | 43.5 | 288 | 3 | US-08-558-135-4 | Sequence 4, Appl |
| 45 | 47 | 43.5 | 288 | 3 | US-08-493-071-1 | Sequence 1, Appl |

ALIGNMENTS

```
RESULT 1
US-08-313-681A-4
Sequence 4, Application US/08313681A
Patent No. 5618675
GENERAL INFORMATION:
APPLICANT: Larrick, James W.
APPLICANT: Wright, Susan C.
APPLICANT: Hirata, Mishimasa
TITLE OF INVENTION: Human Cationic Proteins Having
TITLE OF INVENTION: Lipopolysaccharide Binding and Anti-Coagulant Activity
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,681A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15325-9-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 171 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-313-681A-4
Query Match 100.0%; Score 108; DB 1; Length 171;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 RKRLKFRNKIKKXIGKI 22
DB 137 RKRLKFRNKIKKXIGKI 158
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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:17:55 ; Search time 77.1229 Seconds

(without alignment)
110.327 Million cell updates/sec

Title: US-09-642-744D-21

Sequence: 1 RKRLRKPRNKIKKIKKIGQXI 22

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp19808:*\n2: Geneseqp19908:*\n3: Geneseqp20008:*\n4: Geneseqp20018:*\n5: Geneseqp20028:*\n6: Geneseqp20038:*\n7: Geneseqp20038:*\n8: Geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 108 | 100.0 | 22 | 4 | AAAB70668 |
| 2 | 108 | 100.0 | 24 | 6 | AAE34416 |
| 3 | 108 | 100.0 | 24 | 6 | ADK70763 |
| 4 | 108 | 100.0 | 26 | 6 | AAE34418 |
| 5 | 108 | 100.0 | 26 | 6 | AAE34417 |
| 6 | 108 | 100.0 | 26 | 6 | AAE34419 |
| 7 | 108 | 100.0 | 26 | 6 | AAE34421 |
| 8 | 108 | 100.0 | 26 | 6 | AAE34420 |
| 9 | 108 | 100.0 | 26 | 8 | ADK70762 |
| 10 | 108 | 100.0 | 32 | 3 | AAAB28486 |
| 11 | 108 | 100.0 | 32 | 8 | ADK70761 |
| 12 | 108 | 100.0 | 37 | 4 | AAAB70665 |
| 13 | 108 | 100.0 | 37 | 5 | AAAB70711 |
| 14 | 108 | 100.0 | 37 | 5 | AAAB53272 |
| 15 | 108 | 100.0 | 38 | 4 | AAAB51193 |
| 16 | 108 | 100.0 | 142 | 8 | ADK70796 |
| 17 | 108 | 100.0 | 171 | 5 | AAAB07703 |
| 18 | 104 | 96.3 | 24 | 8 | ADK70764 |
| 19 | 102 | 94.4 | 29 | 2 | AAAR45671 |
| 20 | 102 | 94.4 | 29 | 3 | AAAB07903 |
| 21 | 94 | 87.0 | 21 | 4 | AAAB70666 |
| 22 | 93 | 86.1 | 19 | 4 | AAAB70669 |
| 23 | 93 | 86.1 | 21 | 4 | AAAB70670 |
| 24 | 89 | 82.4 | 18 | 4 | AAAB70667 |
| 25 | 86 | 81.5 | 20 | 8 | ADK70765 |

| | | | | | | | |
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| 26 | 75 | 69.4 | 15 | 4 | AAAB70671 | AAAB70671 | Lupine RC |
| 27 | 70 | 64.8 | 16 | 2 | AAAR45673 | AAAR45673 | RNIP hepa |
| 28 | 70 | 64.8 | 16 | 3 | AAAB07905 | AAAB07905 | Heparin-b |
| 29 | 64 | 59.3 | 31 | 5 | AAO15559 | AAO15559 | Murine ca |
| 30 | 64 | 59.3 | 32 | 5 | AAAB07697 | AAAB07697 | Murine ca |
| 31 | 64 | 59.3 | 33 | 2 | AAAR94449 | AAAR94449 | Murine ant |
| 32 | 64 | 59.3 | 33 | 2 | AAAB53268 | AAAB53268 | Mouse nat |
| 33 | 64 | 59.3 | 173 | 5 | AAAB07701 | AAAB07701 | Murine ca |
| 34 | 62 | 57.4 | 15 | 4 | AAAB70672 | AAAB70672 | Lupine RC |
| 35 | 62 | 57.4 | 17 | 4 | AAAB70673 | AAAB70673 | Lupine RC |
| 36 | 60 | 55.6 | 324 | 8 | ADJ49167 | ADJ49167 | Oil-asso |
| 37 | 60 | 55.6 | 326 | 6 | ADA06238 | ADA06238 | Rape chol |
| 38 | 60 | 55.6 | 326 | 8 | ADU49168 | ADU49168 | Oil-asso |
| 39 | 60 | 55.6 | 326 | 8 | ADOL17009 | ADOL17009 | Breastica |
| 40 | 58 | 53.7 | 36 | 4 | AAAG6421 | AAAG6421 | Mouse cat |
| 41 | 58 | 53.7 | 36 | 5 | AAU09819 | AAU09819 | Mouse cat |
| 42 | 58 | 53.7 | 36 | 5 | ABG31966 | ABG31966 | Mouse cat |
| 43 | 58 | 53.7 | 36 | 5 | ABG31663 | ABG31663 | Mouse cat |
| 44 | 58 | 53.7 | 36 | 5 | AAU76940 | AAU76940 | Mouse cat |
| 45 | 58 | 53.7 | 36 | 6 | ABP58358 | ABP58358 | Mouse cat |

ALIGNMENTS

RESULT 1
AAAB70668
ID AAAB70668 standard; peptide: 22 AA.
XX
AC
XX
AAAB70668;
XX
DT 15-MAY-2001 (first entry)
XX
DE Lupine RCAP 18 cathelicidin derived antimicrobial peptide SEQ ID NO:21.
XX
XX
KM Ovine; SNAP29; lupine; RCAP 18; cathelicidin; antimicrobial;
KM bactericidal; antibiotic; antiviral; microbial growth inhibitor;
KM proliferation inhibitor; gene therapy; Pseudomonas aeruginosa;
KM Burkholderia cepacia; Alcaligenes; Xanthomonas.
XX
OS Oryctolagus cuniculus.
XX
PN WO200112668-A1.
XX
PD 22-FEB-2001.
XX
PF 18-AUG-2000; 2000WO-US022781.
XX
FR 18-AUG-1999; 99US-0149886P.
XX
PA (IOWA) UNIV IOWA RES FOUND.
XX (REGC) UNIV CALIFORNIA.
XX
PI Tack BE, Mccravy P, Welsh M, Travis SM, Lehrer R;
XX WPI; 2001-234911/24.
XX
PT New antimicrobial peptides useful as antibiotics for inhibiting growth
PT and proliferation of microbes, and for treating microbial infections.
XX
PS Claim 1; Page 103; 137pp; English.
XX
CC AAAB70648 to AAAB70675 represent antimicrobial peptides (I) of which
CC AAAB70648 to AAAB70664, AAAB70674 and AAAB70675 are derived from the
CC SNAP 29 cathelicidin family peptide, and AAAB70673 are derived
CC from the lupine RCAP 18 cathelicidin family peptide. (I) have antibiotic,
CC antimicrobial and antiviral activities, and can be used as microbial
CC growth and proliferation inhibitors and in gene therapy. (II) are useful
CC for inhibiting microbial growth in an environment capable of sustaining
CC such growth, for inhibiting microbial growth or strain in a host, and
CC inhibiting the growth of drug-resistant microbial strains such as
CC Pseudomonas aeruginosa, Burkholderia cepacia, Alcaligenes and Xanthomonas

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:17:06 ; Search time 56.162 Seconds

(without alignments)
164.122 Million cell updates/sec

Title: US-09-642-744D-20

Perfect score: 89

Sequence: 1 KRLRRFKIKKIKKIG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 89 | 100.0 | 171 | 1 | CP18_RABIT |
| 2 | 53 | 59.6 | 809 | 2 | P25230 oryctolagus |
| 3 | 51 | 57.3 | 241 | 2 | O6FTT3 |
| 4 | 50 | 56.2 | 166 | 1 | O7G888 |
| 5 | 50 | 56.2 | 173 | 1 | MP36_PIG |
| 6 | 50 | 56.2 | 178 | 2 | CRAM_MOUSE |
| 7 | 50 | 56.2 | 178 | 2 | O60831 |
| 8 | 49 | 55.1 | 142 | 2 | O90T68 |
| 9 | 49 | 55.1 | 241 | 1 | O66881 |
| 10 | 49 | 55.1 | 324 | 1 | 143B_ARATH |
| 11 | 49 | 55.1 | 326 | 2 | O42621 |
| 12 | 49 | 55.1 | 326 | 2 | O42622 |
| 13 | 48 | 53.9 | 113 | 2 | O8GVE3 |
| 14 | 48 | 53.9 | 321 | 2 | O7RA52 |
| 15 | 48 | 53.9 | 364 | 2 | O7RAY0 |
| 16 | 48 | 53.9 | 381 | 2 | O978N0 |
| 17 | 48 | 53.9 | 439 | 2 | O53589 |
| 18 | 48 | 53.9 | 497 | 2 | O8NU03 |
| 19 | 48 | 53.9 | 497 | 2 | O8NUQ3 |
| 20 | 48 | 53.9 | 497 | 2 | O8NUJ3 |
| 21 | 48 | 53.9 | 497 | 2 | O7A3D9 |
| 22 | 48 | 53.9 | 497 | 2 | O6G6B0 |
| 23 | 48 | 53.9 | 497 | 2 | O6GDM5 |
| 24 | 47.5 | 53.4 | 274 | 2 | O48537 |
| 25 | 47.5 | 53.4 | 274 | 2 | O28716 |
| 26 | 47 | 52.8 | 121 | 2 | O67804 |
| 27 | 47 | 52.8 | 141 | 2 | O9NMH7 |
| 28 | 47 | 52.8 | 257 | 1 | O9IEB3 |
| 29 | 47 | 52.8 | 259 | 1 | 1433_CHLRB |
| 30 | 47 | 52.8 | 400 | 2 | O88295 |
| 31 | 47 | 52.8 | 400 | 2 | O88297 |
| | | | | | O89299 |

ALIGNMENTS

| RESULT 1 | CP18_RABIT | STANDARD | PRT | 171 AA. |
|----------|---|----------|-----|---------|
| AC | P25230 | | | |
| DT | 01-MAY-1992 (Rel. 22, Created) | | | |
| DT | 01-MAY-1992 (Rel. 22, Last sequence update) | | | |
| DE | Antimicrobial protein CAP18 precursor (18 kDa lipopolysaccharide-binding protein) (18 kDa cationic protein) (CAP18-A). | | | |
| GN | Name=CAP18; | | | |
| OS | Oryctolagus cuniculus (Rabbit). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus. | | | |
| OX | NCBI_TaxID=9986; | | | |
| LN | [1] | | | |
| RP | SEQUENCE FROM N.A., AND SEQUENCE OF 135-159. | | | |
| RC | TISSUE=bone marrow; | | | |
| RX | MEDLINE=91354246; PubMed=1883348; | | | |
| RA | Larrick J.W., Morgan J.G., Palings I., Hirata M., Yen M.H.; | | | |
| RT | "Complementary DNA sequence of rabbit CAP18 -- a unique lipopolysaccharide binding protein."; | | | |
| RL | Biochem. Biophys. Res. Commun. 179:170-175(1991). | | | |
| RN | [2] | | | |
| RP | SEQUENCE OF 135-159, AND CHARACTERIZATION. | | | |
| RX | MEDLINE=94178952; PubMed=8132348; | | | |
| RA | Hirata M., Shimomura Y., Yoshida M., Morgan J.G., Palings I., | | | |
| RT | Wilson D., Yen M.H., Wright S.C., Larrick J.W.; | | | |
| RL | "Characterization of a rabbit cationic protein (CAP18) with lipopolysaccharide-inhibitory activity."; | | | |
| RN | Infect. Immun. 62:1421-1426(1994). | | | |
| RP | [3] | | | |
| RX | SEQUENCE OF 135-154, AND CHARACTERIZATION. | | | |
| RA | MEDLINE=94075827; PubMed=8254193; | | | |
| RT | Larrick J.W., Hirata M., Zheng H., Zhong J., Bolin D., | | | |
| RL | "A novel granulocyte-derived peptide with lipopolysaccharide-neutralizing activity."; | | | |
| RN | J. Immunol. 152:231-240(1994). | | | |
| RP | [4] | | | |
| RX | CHARACTERIZATION. | | | |
| RA | MEDLINE=94148064; PubMed=8133956; DOI=10.1016/0014-5793(94)80395-1; | | | |
| RT | Tobai A., Scocchi M., Skerlavaj B., Gennaro R.; | | | |
| RL | "Identification and characterization of a primary antibacterial domain in CAP18, a lipopolysaccharide binding protein from rabbit leukocytes."; | | | |
| RN | FEBS Lett. 339:108-112(1994). | | | |
| RP | [5] | | | |
| RX | STRUCTURE BY NMR OF 135-166. | | | |
| RA | MEDLINE=95377455; PubMed=7649303; DOI=10.1016/0014-5793(95)00792-8; | | | |
| RT | Chen C., Brock R., Luh F., Chou P.-J., Larrick J.W., Huang R.-F., | | | |
| RL | Huang T.-H.; | | | |
| RT | "The solution structure of the active domain of CAP18 -- a lipopolysaccharide binding protein from rabbit leukocytes."; | | | |
| RL | FEBS Lett. 370:46-52(1995). | | | |

| | | | | | | |
|----|----|------|------|---|-------------|--------------------------|
| 32 | 47 | 52.8 | 400 | 2 | O89304 | O89304 yellow fever |
| 33 | 47 | 52.8 | 400 | 2 | O89311 | O89311 yellow fever |
| 34 | 47 | 52.8 | 400 | 2 | O89315 | O89315 yellow fever |
| 35 | 47 | 52.8 | 400 | 2 | O89317 | O89317 yellow fever |
| 36 | 47 | 52.8 | 511 | 2 | O89319 | O89319 fusobacteri |
| 37 | 47 | 52.8 | 778 | 2 | O7PB05 | O7PB05 yellow fever |
| 38 | 47 | 52.8 | 778 | 2 | O77X62 | O77X62 yellow fever |
| 39 | 47 | 52.8 | 778 | 2 | O77X64 | O77X64 yellow fever |
| 40 | 47 | 52.8 | 778 | 2 | O9W9B8 | O9W9B8 yellow fever |
| 41 | 47 | 52.8 | 1163 | 1 | POLG_YERF8 | POLG_YERF8 yellow fever |
| 42 | 47 | 52.8 | 1300 | 2 | O7RB01 | O7RB01 plasmodium |
| 43 | 47 | 52.8 | 1321 | 2 | O8IBV4 | O8IBV4 plasmodium |
| 44 | 47 | 52.8 | 1335 | 1 | SOJO_XENTIA | SOJO_XENTIA plasmodium |
| 45 | 47 | 52.8 | 3411 | 1 | POLG_YERFV1 | POLG_YERFV1 yellow fever |
| | | | | | | P03314 Y genome po |

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:21:40 ; Search time 11.162 Seconds

(without alignments)
155.160 Million cell updates/sec

Title: US-09-642-744D-20

Sequence: 1 KRLKFRNKIKKKKIG 18

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.79:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 89 | 100.0 | 171 | 2 JQ1171 | 18K lipopolysaccha |
| 2 | 51 | 57.3 | 241 | 2 G86355 | antibacterial prote |
| 3 | 50 | 56.2 | 166 | 2 S41731 | cathelin-related p |
| 4 | 50 | 56.2 | 173 | 2 S70521 | hypothetical prote |
| 5 | 49 | 55.1 | 142 | 2 E70356 | probable choline-p |
| 6 | 49 | 55.1 | 324 | 2 T07982 | choline-phosphate |
| 7 | 49 | 55.1 | 326 | 2 T07983 | hypothetical prote |
| 8 | 48 | 53.9 | 497 | 2 B90061 | conserved hypochet |
| 9 | 47.5 | 53.4 | 274 | 2 C69444 | conserved hypochet |
| 10 | 47 | 52.8 | 121 | 2 H70471 | 14-3-3 brain prote |
| 11 | 47 | 52.8 | 259 | 2 S57283 | genome polypeptid |
| 12 | 47 | 52.8 | 1163 | 1 GNMVY8 | genome polypeptid |
| 13 | 47 | 52.8 | 3411 | 1 GNMVY | genome polypeptid |
| 14 | 47 | 52.8 | 3411 | 1 GNMVY | genome polypeptid |
| 15 | 46 | 51.7 | 169 | 2 A82373 | polypeptide defor |
| 16 | 46 | 51.7 | 305 | 2 T23929 | hypothetical prote |
| 17 | 46 | 51.7 | 329 | 2 T07981 | probable choline-p |
| 18 | 46 | 51.7 | 331 | 2 T07980 | hypothetical prote |
| 19 | 46 | 51.7 | 444 | 2 T24844 | probable choline-p |
| 20 | 46 | 51.7 | 984 | 2 D70461 | hypothetical prote |
| 21 | 46 | 51.7 | 996 | 1 S42208 | preprotein transla |
| 22 | 45.5 | 51.1 | 661 | 2 T37753 | NAD ADP-ribosyltra |
| 23 | 45 | 50.6 | 153 | 2 JN0344 | hypothetical prote |
| 24 | 45 | 50.6 | 174 | 2 F84426 | myoglobin - Baikal |
| 25 | 45 | 50.6 | 453 | 2 B72500 | hypothetical prote |
| 26 | 45 | 50.6 | 522 | 2 A95059 | probable seryl-tRN |
| 27 | 45 | 50.6 | 522 | 2 H97927 | hypothetical prote |
| 28 | 45 | 50.6 | 655 | 2 S57119 | type 1 site-specif |
| 29 | 45 | 50.6 | 831 | 2 S44843 | hypothetical prote |

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| 30 | 45 | 50.6 | 1233 | 2 I54383 | chromosome segrega |
| 31 | 44.5 | 50.0 | 458 | 2 D70410 | cytosolic axial fi |
| 32 | 44 | 49.4 | 96 | 2 H69042 | ribosomal protein |
| 33 | 44 | 49.4 | 109 | 2 G64379 | hypothetical prote |
| 34 | 44 | 49.4 | 184 | 2 T04396 | Richs protein - ba |
| 35 | 44 | 49.4 | 254 | 2 H86355 | probable 14-3-3 pr |
| 36 | 44 | 49.4 | 288 | 2 UN0466 | epimorphin - human |
| 37 | 44 | 49.4 | 298 | 2 E85166 | probable phosphoch |
| 38 | 44 | 49.4 | 425 | 2 T24111 | hypothetical prote |
| 39 | 44 | 49.4 | 894 | 2 T15769 | hypothetical prote |
| 40 | 43.5 | 48.9 | 477 | 2 A75052 | cysteiny1-cRNA syn |
| 41 | 43.5 | 48.9 | 573 | 2 D90202 | methionyl-cRNA syn |
| 42 | 43.5 | 48.9 | 966 | 2 B84481 | hypothetical prote |
| 43 | 43 | 48.3 | 73 | 2 T03182 | hypothetical prote |
| 44 | 43 | 48.3 | 96 | 2 F72228 | ribosomal protein |
| 45 | 43 | 48.3 | 119 | 2 C90351 | hypothetical prote |

ALIGNMENTS

RESULT 1

JQ1171

18K lipopolysaccharide-binding protein precursor - rabbit

N/Alternate names: 18K cationic protein

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #ext_change 06-Dec-1996

C/Accession: JQ1171; PS0226

R/Larick, J.W.; Morgan, J.G.; Palling, I.; Hirata, M.; Yen, M.H.

Biochem. Biophys. Res. Commun. 179, 170-175, 1991

A/Title: Complementary DNA sequence of rabbit CAP18-a unique lipopolysaccharide binding

A/Reference number: JQ1171; PMID:91354246; PMID:1883448

A/Accession: JQ1171

A/Molecule type: mRNA

A/Residues: 1-171 <LA>

A/Experimental source: bone marrow

A/Accession: PS0226

A/Molecule type: protein

A/Residues: 135-159, 'QIGQL' <LA2>

A/Note: 157-Asp was also found

C/Superfamily: cathelin; cystatin homology

F/1-29/Domain: signal sequence #status predicted <SIG>

F/30-111/Product: 18K lipopolysaccharide-binding protein #status predicted <MAT>

Query Match 100.0%; Score 89; DB 2; Length 171;

Best Local Similarity 100.0%; Pred. No. 9.2e-05;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KRLKFRNKIKKKKIG 18

Db 138 KRLKFRNKIKKKKIG 155

RESULT 2

G86355

hypothetical protein T16E15.9 - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #ext_change 31-Dec-2001

C/Accession: G86355

R/Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso

Chin, C.W.; Chung, M.K.; Corn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.

ansen, N.F.; Hughes, B.; Huizar, L.

A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Malt, R.; Marshall

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A/Reference number: A66141; MUID:21016719; PMID:11130712

A/Accession: G86355

A/status: preliminary

A/molecule type: DNA

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 2, 2005, 13:03:56 ; Search time 48.9721 Seconds

(Without alignments)
122.435 Million cell updates/sec

Title: US-09-642-744D-20

Sequence: 1 KRLRKFRNKIKKIKIG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1426032 seqs, 333106140 residues

Total number of hits satisfying chosen parameters: 1426032

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/1/pubppa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubppa/PCT_NEW_PUB.pep.*
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8: /cgn2_6/ptodata/1/pubppa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubppa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubppa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubppa/US09C_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubppa/US10C_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 3 | 89 | 100.0 | 37 | 15 | US-10-721-839-5 |
| 4 | 89 | 100.0 | 37 | 15 | US-10-344-709C-15 |
| 5 | 89 | 100.0 | 171 | 16 | US-10-344-709C-7 |
| 6 | 50 | 56.2 | 31 | 17 | US-10-344-709C-1 |
| 7 | 50 | 56.2 | 32 | 16 | US-10-344-709C-2 |
| 8 | 50 | 56.2 | 35 | 13 | US-10-205-150-1 |
| 9 | 50 | 56.2 | 35 | 14 | US-10-269-171A-2 |
| 10 | 50 | 56.2 | 36 | 17 | US-10-470-048B-599 |
| 11 | 50 | 56.2 | 39 | 14 | US-10-060-102-1 |
| 12 | 50 | 56.2 | 39 | 15 | US-10-721-839-1 |
| 13 | 50 | 56.2 | 155 | 15 | US-10-336-603A-34 |

| | | | | | | |
|----|----|------|-----|----|----------------------|--------------------|
| 14 | 50 | 56.2 | 173 | 16 | US-10-344-709C-5 | Sequence 5, Appl1 |
| 15 | 50 | 56.2 | 178 | 13 | US-10-015-179-2 | Sequence 2, Appl1 |
| 16 | 50 | 56.2 | 178 | 15 | US-10-188-840-2 | Sequence 2, Appl1 |
| 17 | 50 | 56.2 | 178 | 15 | US-10-336-603A-32 | Sequence 32, Appl1 |
| 18 | 50 | 56.2 | 258 | 9 | US-09-828-447-13 | Sequence 13, Appl1 |
| 19 | 49 | 55.1 | 324 | 15 | US-10-389-566-1171 | Sequence 1171, Ap |
| 20 | 49 | 55.1 | 326 | 14 | US-10-233-926-25 | Sequence 25, Appl1 |
| 21 | 49 | 55.1 | 326 | 15 | US-10-389-566-1172 | Sequence 1172, Ap |
| 22 | 48 | 53.9 | 51 | 15 | US-10-424-559-264915 | Sequence 264915, |
| 23 | 48 | 53.9 | 51 | 15 | US-10-424-559-264915 | Sequence 264915, |
| 24 | 48 | 53.9 | 49 | 15 | US-09-815-242-5696 | Sequence 5696, Ap |
| 25 | 48 | 53.9 | 49 | 9 | US-10-358-917-14 | Sequence 14, Appl1 |
| 26 | 48 | 53.9 | 49 | 14 | US-10-282-122A-43955 | Sequence 43955, A |
| 27 | 47 | 52.8 | 443 | 16 | US-10-757-701-44345 | Sequence 44345, A |
| 28 | 47 | 52.8 | 881 | 15 | US-10-282-122A-52884 | Sequence 52884, A |
| 29 | 46 | 51.7 | 123 | 9 | US-09-820-893-81 | Sequence 81, Appl1 |
| 30 | 46 | 51.7 | 123 | 9 | US-09-820-893-92 | Sequence 92, Appl1 |
| 31 | 46 | 51.7 | 123 | 9 | US-09-811-876-187 | Sequence 187, App |
| 32 | 46 | 51.7 | 123 | 9 | US-09-811-876-243 | Sequence 243, App |
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| 35 | 46 | 51.7 | 123 | 15 | US-10-607-565-81 | Sequence 81, Appl1 |
| 36 | 46 | 51.7 | 123 | 15 | US-10-607-565-92 | Sequence 92, Appl1 |
| 37 | 46 | 51.7 | 169 | 14 | US-10-197-666A-58 | Sequence 58, Appl1 |
| 38 | 46 | 51.7 | 188 | 9 | US-09-820-893-57 | Sequence 57, Appl1 |
| 39 | 46 | 51.7 | 188 | 14 | US-10-197-666A-54 | Sequence 54, Appl1 |
| 40 | 46 | 51.7 | 188 | 15 | US-10-607-565-57 | Sequence 57, Appl1 |
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| 42 | 46 | 51.7 | 329 | 14 | US-10-233-926-24 | Sequence 24, Appl1 |
| 43 | 46 | 51.7 | 329 | 15 | US-10-389-566-1173 | Sequence 1173, Ap |
| 44 | 46 | 51.7 | 331 | 14 | US-10-233-926-23 | Sequence 23, Appl1 |
| 45 | 46 | 51.7 | 331 | 15 | US-10-389-566-1174 | Sequence 1174, Ap |

ALIGNMENTS

RESULT 1
US-10-131-433-1
Sequence 1, Application US/10131433
Publication No. US20030054422A1
GENERAL INFORMATION:
APPLICANT: UNILEVER, PLC
TITLE OF INVENTION: Lipopolysaccharide Immunoassay and Test Device
FILE REFERENCE: Lipopolysaccharide Immunoassay
CURRENT APPLICATION NUMBER: US/10/131,433
PRIOR FILING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: US/09/545,180
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 32
TYPE: PRT
ORGANISM: Lactine
US-10-131-433-1

Query Match
Best Local Similarity 100.0%; Score 89; DB 14; Length 32;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KRLRKFRNKIKKIKIG 18
Db 4 KRLRKFRNKIKKIKIG 21

RESULT 2
US-10-060-102-5
Sequence 5, Application US/10060102
Publication No. US20030022829A1
GENERAL INFORMATION:
APPLICANT: MAURY, WENDY
APPLICANT: STAPLETON, JACK

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:18:40 ; Search time 17.095 Seconds

(without alignments)
78,601 Million cell updates/sec

Title: US-09-642-744d-20

Sequence: 1 KRLRRFKRKIKKKIG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 segs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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5: /cgn2_6/ptodata/1/1aa/PCTUS.COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 3 | 89 | 100.0 | 171 | 1 US-08-313-681A-4 | Sequence 4, Appli |
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| 8 | 50 | 56.2 | 258 | 4 US-09-828-447-13 | Sequence 13, Appli |
| 9 | 49 | 55.1 | 18 | 4 US-09-525-269A-10 | Sequence 10, Appli |
| 10 | 49 | 55.1 | 326 | 4 US-09-735-846-25 | Sequence 25, Appli |
| 11 | 49 | 55.1 | 452 | 4 US-09-889-738-21 | Sequence 21, Appli |
| 12 | 47 | 52.8 | 3421 | 4 US-09-452-638-53 | Sequence 53, Appli |
| 13 | 46 | 51.7 | 18 | 1 US-07-725-331-29 | Sequence 29, Appli |
| 14 | 46 | 51.7 | 18 | 5 PCT-US91-05047-29 | Sequence 29, Appli |
| 15 | 46 | 51.7 | 123 | 4 US-09-148-545-187 | Sequence 187, App |
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| 19 | 46 | 51.7 | 331 | 4 US-09-735-846-23 | Sequence 23, Appli |
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| 21 | 45 | 50.6 | 269 | 4 US-09-744-989C-3 | Sequence 3, Appli |
| 22 | 45 | 50.6 | 287 | 4 US-09-744-989C-1 | Sequence 1, Appli |
| 23 | 45 | 50.6 | 287 | 4 US-09-744-989C-5 | Sequence 5, Appli |
| 24 | 45 | 50.6 | 429 | 4 US-09-583-110-4660 | Sequence 4660, Ap |
| 25 | 45 | 50.6 | 531 | 4 US-09-107-433-5016 | Sequence 5016, Ap |
| 26 | 45 | 50.6 | 726 | 4 US-09-252-991A-26767 | Sequence 26767, A |
| 27 | 45 | 50.6 | 1244 | 4 US-09-949-016-11702 | Sequence 11702, A |

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| 28 | 44 | 49.4 | 96 | 4 US-09-732-210-707 | Sequence 707, App |
| 29 | 44 | 49.4 | 103 | 3 US-09-308-388-1 | Sequence 1, Appli |
| 30 | 44 | 49.4 | 187 | 3 US-08-493-071-16 | Sequence 16, Appli |
| 31 | 44 | 49.4 | 236 | 3 US-08-493-071-15 | Sequence 15, Appli |
| 32 | 44 | 49.4 | 277 | 1 US-08-690-457-5 | Sequence 5, Appli |
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| 35 | 44 | 49.4 | 287 | 1 US-08-690-457-4 | Sequence 4, Appli |
| 36 | 44 | 49.4 | 287 | 2 US-08-628-187-4 | Sequence 4, Appli |
| 37 | 44 | 49.4 | 287 | 3 US-08-493-071-2 | Sequence 2, Appli |
| 38 | 44 | 49.4 | 288 | 1 US-08-690-457-3 | Sequence 3, Appli |
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| 42 | 43 | 48.3 | 18 | 1 US-07-725-331-27 | Sequence 27, Appli |
| 43 | 43 | 48.3 | 18 | 5 PCT-US91-05047-24 | Sequence 24, Appli |
| 44 | 43 | 48.3 | 18 | 5 PCT-US91-05047-27 | Sequence 27, Appli |
| 45 | 43 | 48.3 | 158 | 4 US-09-107-532A-5475 | Sequence 5475, Ap |

ALIGNMENTS

RESULT 1
US-08-313-681A-7
Sequence 7, Application US/08313681A
Patent No. 5618675
GENERAL INFORMATION:
APPLICANT: Larrick, James W.
APPLICANT: Wright, Susan C.
APPLICANT: Hirata, Miehlmasa
TITLE OF INVENTION: Human Cationic Proteins Having
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Hourie and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,681A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15325-9-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Region
LOCATION: 23
OTHER INFORMATION: /note= "Xaa is Asp or Lys"
FEATURE:
NAME/KEY: Region
LOCATION: 26
OTHER INFORMATION: /note= "Xaa is a Gln or Ile"

GenCore Version 5.1.6
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OM protein - protein search, using BW model

Run on: May 2, 2005, 13:03:56 ; Search time 57.1341 Seconds

(without alignments)
122.435 Million cell updates/sec

Title: US-09-642-744d-19

Perfect score: 104

Sequence: 1 GRRRLRRFRNKIKKKKIG 21

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1426032 seqs, 333106140 residues

Total number of hits satisfying chosen parameters: 1426032

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 2 | 104 | 100.0 | 37 | 14 | US-10-060-102-5 |
| 3 | 104 | 100.0 | 37 | 15 | US-10-721-839-5 |
| 4 | 104 | 100.0 | 37 | 16 | US-10-344-709C-15 |
| 5 | 104 | 100.0 | 171 | 16 | US-10-344-709C-7 |
| 6 | 53.5 | 51.4 | 112 | 16 | US-10-767-701-35738 |
| 7 | 51.5 | 49.5 | 976 | 15 | US-10-282-122A-51750 |
| 8 | 51 | 49.0 | 334 | 15 | US-10-094-749-2450 |
| 9 | 51 | 49.0 | 334 | 16 | US-10-471-450-20 |
| 10 | 51 | 49.0 | 641 | 16 | US-10-437-963-181519 |
| 11 | 50 | 48.1 | 31 | 17 | US-10-399-442A-2 |
| 12 | 50 | 48.1 | 32 | 16 | US-10-344-709C-1 |
| 13 | 50 | 48.1 | 35 | 13 | US-10-205-150-1 |

| | | | | | | |
|----|------|------|------|----|----------------------|--------------------|
| 14 | 50 | 48.1 | 36 | 14 | US-10-269-171A-2 | Sequence 2, Appl1 |
| 15 | 50 | 48.1 | 36 | 17 | US-10-470-048B-599 | Sequence 599, App |
| 16 | 50 | 48.1 | 39 | 14 | US-10-060-102-1 | Sequence 1, Appl1 |
| 17 | 50 | 48.1 | 39 | 15 | US-10-721-839-1 | Sequence 1, Appl1 |
| 18 | 50 | 48.1 | 51 | 15 | US-10-424-599-264915 | Sequence 264915, |
| 19 | 50 | 48.1 | 51 | 15 | US-10-424-599-243585 | Sequence 243585, |
| 20 | 50 | 48.1 | 155 | 15 | US-10-336-603A-34 | Sequence 34, Appl1 |
| 21 | 50 | 48.1 | 173 | 16 | US-10-344-709C-5 | Sequence 3, Appl1 |
| 22 | 50 | 48.1 | 178 | 13 | US-10-015-179-2 | Sequence 2, Appl1 |
| 23 | 50 | 48.1 | 178 | 15 | US-10-188-840-2 | Sequence 13, Appl1 |
| 24 | 50 | 48.1 | 178 | 15 | US-10-336-603A-32 | Sequence 65, Appl1 |
| 25 | 50 | 48.1 | 258 | 9 | US-09-828-447-13 | Sequence 65, Appl1 |
| 26 | 49.5 | 47.6 | 932 | 14 | US-10-126-927-65 | Sequence 1171, Ap |
| 27 | 49.5 | 47.6 | 932 | 14 | US-10-126-931A-75 | Sequence 25, Appl1 |
| 28 | 49 | 47.1 | 324 | 15 | US-10-389-566-1171 | Sequence 1172, Ap |
| 29 | 49 | 47.1 | 326 | 14 | US-10-233-928-25 | Sequence 184641, |
| 30 | 49 | 47.1 | 326 | 15 | US-10-389-566-1172 | Sequence 52425, A |
| 31 | 49 | 47.1 | 333 | 15 | US-10-424-599-184641 | Sequence 36970, A |
| 32 | 49 | 47.1 | 386 | 15 | US-10-425-114-52425 | Sequence 202825, |
| 33 | 49 | 47.1 | 394 | 15 | US-10-425-114-36970 | Sequence 1, Appl1 |
| 34 | 48 | 46.2 | 67 | 15 | US-10-424-599-202825 | Sequence 1, Appl1 |
| 35 | 48 | 46.2 | 103 | 14 | US-10-155-922-1 | Sequence 5696, Ap |
| 36 | 48 | 46.2 | 103 | 17 | US-10-754-079-1 | Sequence 14, Appl1 |
| 37 | 48 | 46.2 | 439 | 9 | US-09-815-242-5696 | Sequence 43955, A |
| 38 | 48 | 46.2 | 497 | 14 | US-10-358-917-14 | Sequence 193298, |
| 39 | 48 | 46.2 | 497 | 15 | US-10-282-122A-43955 | Sequence 44345, A |
| 40 | 47 | 45.2 | 73 | 15 | US-10-424-599-193298 | Sequence 52284, A |
| 41 | 47 | 45.2 | 443 | 16 | US-10-767-701-44345 | Sequence 1566, App |
| 42 | 47 | 45.2 | 881 | 15 | US-10-282-122A-52284 | Sequence 154242, |
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| 44 | 46.5 | 44.7 | 350 | 16 | US-10-437-963-154242 | |
| 45 | 46 | 44.2 | 68 | 16 | US-10-437-963-163080 | |

ALIGNMENTS

RESULT 1

US-10-131-433-1

Sequence 1, Application US/10131433

Publication No. US20030054422A1

GENERAL INFORMATION:

APPLICANT: UNILEVER, PLC

TITLE OF INVENTION: Lipopolysaccharide Immunoassay and Test Device

FILE REFERENCE: Lipopolysaccharide Immunoassay

CURRENT APPLICATION NUMBER: US/10/131,433

CURRENT FILING DATE: 2002-04-23

PRIOR APPLICATION NUMBER: US/09/545,180

PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ ID NOS: 8

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1

LENGTH: 32

TYPE: PRT

ORGANISM: Lاپine

US-10-131-433-1

Query Match

Best Local Similarity 100.0%; Score 104; DB 14; Length 32;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db

1 GRRRLRRFRNKIKKKKIG 21

US-10-060-102-5

Sequence 5, Appl1

Publication No. US20030022829A1

GENERAL INFORMATION:

APPLICANT: MAURY, WENDY

APPLICANT: STAPLETON, JACK

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:18:40 / Search time 19.9441 Seconds
(without alignments)
78.601 Million cell updates/sec

Title: US-09-642-744D-19
Perfect score: 104
Sequence: 1 GURKRLRKFRNKIKKKIG 21

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 8 | 50 | 48.1 | 33 | 5 US-09-452-638-53 | Sequence 53, Appl |
| 9 | 50 | 48.1 | 33 | 5 PCT-US95-12080-4 | Sequence 53, Appl |
| 10 | 49 | 47.1 | 18 | 4 US-09-828-447-13 | Sequence 13, Appl |
| 11 | 49 | 47.1 | 37 | 4 US-09-525-269A-10 | Sequence 10, Appl |
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| 14 | 49 | 47.1 | 245 | 4 US-09-543-681A-6428 | Sequence 6428, Ap |
| 15 | 49 | 47.1 | 269 | 4 US-09-744-989C-3 | Sequence 3, Appl |
| 16 | 49 | 47.1 | 287 | 4 US-09-744-989C-1 | Sequence 1, Appl |
| 17 | 49 | 47.1 | 287 | 4 US-09-744-989C-5 | Sequence 5, Appl |
| 18 | 49 | 47.1 | 326 | 4 US-09-735-846-25 | Sequence 25, Appl |
| 19 | 49 | 47.1 | 452 | 4 US-09-889-738-21 | Sequence 21, Appl |
| 20 | 48 | 46.2 | 103 | 3 US-09-308-388-1 | Sequence 1, Appl |
| 21 | 48 | 46.2 | 236 | 3 US-08-493-071-15 | Sequence 15, Appl |
| 22 | 48 | 46.2 | 277 | 2 US-08-690-457-5 | Sequence 5, Appl |
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| 24 | 48 | 46.2 | 277 | 3 US-08-493-071-3 | Sequence 3, Appl |
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| 26 | 48 | 46.2 | 287 | 3 US-08-628-187-4 | Sequence 4, Appl |
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| | | | | 1 US-08-690-457-3 | Sequence 3, Appl |

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| 28 | 48 | 46.2 | 288 | 2 US-08-628-187-3 | Sequence 3, Appl |
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| 31 | 47 | 45.2 | 189 | 4 US-09-134-000C-4590 | Sequence 4590, Ap |
| 32 | 47 | 45.2 | 223 | 4 US-09-344-624-12 | Sequence 12, Appl |
| 33 | 47 | 45.2 | 1244 | 4 US-09-949-016-11702 | Sequence 11702, A |
| 34 | 46 | 44.2 | 18 | 5 PCT-US91-05047-29 | Sequence 29, Appl |
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| 36 | 46 | 44.2 | 123 | 4 US-09-148-545-187 | Sequence 187, App |
| 37 | 46 | 44.2 | 123 | 4 US-09-148-545-187 | Sequence 243, App |
| 38 | 46 | 44.2 | 188 | 4 US-09-695-795A-6 | Sequence 6, Appl |
| 39 | 46 | 44.2 | 329 | 4 US-09-735-846-24 | Sequence 23, Appl |
| 40 | 46 | 44.2 | 331 | 4 US-08-942-572-23 | Sequence 23, Appl |
| 41 | 46 | 44.2 | 413 | 3 US-08-942-572-23 | Sequence 24, Appl |
| 42 | 46 | 44.2 | 413 | 4 US-09-614-068-13 | Sequence 2, Appl |
| 43 | 46 | 44.2 | 413 | 4 US-09-614-068-13 | Sequence 13, Appl |
| 44 | 46 | 44.2 | 413 | 4 US-09-821-803A-7 | Sequence 14, Appl |
| 45 | 46 | 44.2 | 413 | 4 US-09-821-803A-8 | Sequence 7, Appl |
| 46 | 46 | 44.2 | 413 | 4 US-09-821-803A-8 | Sequence 8, Appl |

ALIGNMENTS

RESULT 1
US-08-313-681A-7
Sequence 7, Application US/08313681A
Patent No. 5618675
GENERAL INFORMATION:
APPLICANT: Larrick, James W.
APPLICANT: Wright, Susan C.
APPLICANT: Hirata, Mishima
TITLE OF INVENTION: Human Cationic Proteins Having
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Hourie and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,681A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET INFORMATION: 15325-9-1
TELECOMMUNICATION INFORMATION: 15325-9-1
TELEPHONE: 415-326-2420
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Region
LOCATION: 23
OTHER INFORMATION: /note= "Xaa is Asp or Lys"
FEATURE:
NAME/KEY: Region
LOCATION: 26
OTHER INFORMATION: /note= "Xaa is a Gln or Ile"

GenCore version 5.1.6
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Run on: May 2, 2005, 12:17:55 ; Search time 73.6173 Seconds
(without alignments)
110.327 Million cell updates/sec

Title: US-09-642-744d-19

Perfect score: 104
Sequence: 1 GIKRKLRFKRNKIKLKKIG 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: Geneseqp20028:.*
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8: Geneseqp20058:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 3 | 104 | 100.0 | 24 | 8 ADK70763 | Adk70763 Rabbit CA |
| 4 | 104 | 100.0 | 24 | 8 ADK70764 | Adk70764 Rabbit CA |
| 5 | 104 | 100.0 | 26 | 6 AAE34418 | Aae34418 Rabbit CA |
| 6 | 104 | 100.0 | 26 | 6 AAE34417 | Aae34417 Rabbit CA |
| 7 | 104 | 100.0 | 26 | 6 AAE34419 | Aae34419 Rabbit CA |
| 8 | 104 | 100.0 | 26 | 6 AAE34421 | Aae34421 Rabbit CA |
| 9 | 104 | 100.0 | 26 | 6 AAE34420 | Aae34420 Rabbit CA |
| 10 | 104 | 100.0 | 26 | 8 ADK70762 | Adk70762 Rabbit CA |
| 11 | 104 | 100.0 | 29 | 2 AAR45671 | Aar45671 N terminu |
| 12 | 104 | 100.0 | 29 | 3 AAB70903 | Aab70903 Putative |
| 13 | 104 | 100.0 | 32 | 3 AAB28486 | Aab28486 Rabbit 11 |
| 14 | 104 | 100.0 | 32 | 8 AAB70761 | Adk70761 Rabbit CA |
| 15 | 104 | 100.0 | 37 | 5 AAB70665 | Aab70665 Lupine RC |
| 16 | 104 | 100.0 | 37 | 5 ABB07711 | Abb07711 Antimicro |
| 17 | 104 | 100.0 | 37 | 5 ABB53272 | Abp53272 Sheep nat |
| 18 | 104 | 100.0 | 38 | 4 AAB51193 | Aab51193 E. coli A |
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| 21 | 98 | 94.2 | 20 | 8 AAB70675 | Adk70765 Rabbit pe |
| 22 | 94 | 90.4 | 22 | 4 AAB70668 | Aab70668 Lupine CA |
| 23 | 89 | 85.6 | 18 | 4 AAB70667 | Aab70667 Lupine RC |
| 24 | 80 | 76.9 | 16 | 2 AAR45673 | Aar45673 RNP hepa |
| 25 | 80 | 76.9 | 16 | 3 AAB07905 | Aab07905 Heparin-b |

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| 26 | 79 | 76.0 | 19 | 4 AAB70669 | Aab70669 Lupine RC |
| 27 | 79 | 76.0 | 21 | 4 AAB70670 | Aab70670 Lupine RC |
| 28 | 75 | 72.1 | 15 | 4 AAB70671 | Aab70671 Lupine RC |
| 29 | 53 | 51.0 | 3411 | 8 ADJ57394 | Adj57394 Hamster p |
| 30 | 53 | 51.0 | 3421 | 4 AAB84902 | Aab84902 Chimeric |
| 31 | 51.5 | 49.5 | 976 | 6 AEU23826 | Abu23826 Protein e |
| 32 | 51 | 49.0 | 228 | 8 ADK16769 | Adk16769 Nanoarcha |
| 33 | 51 | 49.0 | 334 | 5 AAG95663 | Abg95663 Human nuc |
| 34 | 51 | 49.0 | 334 | 6 ADA54882 | Ada54882 Human pro |
| 35 | 51 | 49.0 | 365 | 6 ABR41394 | Abt41394 Human DIT |
| 36 | 50 | 48.1 | 31 | 5 AAO15559 | Aao15559 Murine DIT |
| 37 | 50 | 48.1 | 32 | 5 ABB07697 | Abb07697 Murine ca |
| 38 | 50 | 48.1 | 33 | 2 AAR94449 | Aar94449 Murine ant |
| 39 | 50 | 48.1 | 35 | 8 ADR84033 | Adr84033 Murine ca |
| 40 | 50 | 48.1 | 36 | 4 AAG66421 | Aag66421 Mouse cat |
| 41 | 50 | 48.1 | 36 | 5 AAU09819 | Aau09819 Mouse cat |
| 42 | 50 | 48.1 | 36 | 5 AAG31966 | Abg31966 Mouse cat |
| 43 | 50 | 48.1 | 36 | 5 ABG31663 | Abg31663 Mouse cat |
| 44 | 50 | 48.1 | 36 | 5 AAU76940 | Aau76940 Mouse cat |
| 45 | 50 | 48.1 | 36 | 6 ABP58358 | Abp58358 Mouse cat |

ALIGNMENTS

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ID AAB70666 standard; peptide; 21 AA.
XX
AC AAB70666;
XX
DT 15-MAY-2001 (first entry)
XX
DE Lupine RCAP 18 cathelicidin derived antimicrobial peptide SEQ ID NO:19.
XX
KW Ovine; SMAP29; lupine; RCAP 18; cathelicidin; antimicrobial;
KW bactericidal; antibiotic; antiviral; microbial growth inhibitor;
KW proliferation inhibitor; gene therapy; Pseudomonas aeruginosa;
KW Burkholderia cepacia; Alcaligenes; Xanthomonas.
XX
OS Oryctolagus cuniculus.
XX
PN NO200112668-A1.
XX
PD 22-FEB-2001.
XX
PF 18-AUG-2000; 2000MO-US022781.
XX
PR 18-AUG-1999; 99US-0149886P.
XX
PA (IOWA) UNIV IOWA RES FOUND.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Tack BE, Mccray P, Welsh M, Travis SM, Lehrer R;
XX
DR WPI; 2001-234911/24.
XX
XX New antimicrobial peptides useful as antibiotics for inhibiting growth
XX and proliferation of microbes, and for treating microbial infections.
XX
PS Claim 1, Page 103; 137p; English.
XX
CC AAB70648 to AAB70675 represent antimicrobial peptides (I), of which
CC AAB70648 to AAB70664, AAB70674 and AAB70675 are derived from the ovine
CC SMAP 29 cathelicidin family peptide, and AAB70665 to AAB70673 are derived
CC from the lupine RCAP 18 cathelicidin family peptide. (I) have antibiotic,
CC antimicrobial and antiviral activities, and can be used as microbial
CC growth and proliferation inhibitors and in gene therapy. (II) are useful
CC for inhibiting microbial growth in an environment capable of sustaining
CC such growth, for inhibiting microbial growth or strain in a host, and
CC inhibiting the growth of drug-resistant microbial strains such as
CC Pseudomonas aeruginosa, Burkholderia cepacia, Alcaligenes and Xanthomonas

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 2, 2005, 12:17:06 ; Search time 37.4413 Seconds
(without alignments)

164.122 Million cell updates/sec

Title: US-09-642-744d-17
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Sequence: 1 RRIKRIHIIK 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: uniprot_sprot.*
2: uniprot_tramb1.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 3 | 40 | 70.2 | 414 | 0947U2 | O89A21 oryza sativ |
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| 5 | 39 | 68.4 | 202 | HAM1_AQUAB | O66580 agulifex aeo |
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| 7 | 39 | 68.4 | 4057 | 081JY7 | O81JY7 bordetella |
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| 15 | 38 | 66.7 | 623 | Y014_MYCPN | P75095 mycoplasma |
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| 31 | 37 | 64.9 | 491 | 09H8X2 | O9H8X2 homo sapien |

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| 34 | 36 | 63.2 | 113 | 2 | O6J4F4 | O6J4F4 neodipion |
| 35 | 36 | 63.2 | 175 | 2 | 07WNH8 | O7WNH8 bordetella |
| 36 | 36 | 63.2 | 244 | 2 | 07VQO3 | O7VQO3 candidatus |
| 37 | 36 | 63.2 | 284 | 2 | 08XGZ9 | O8XGZ9 salmonella |
| 38 | 36 | 63.2 | 284 | 2 | 07CPQ7 | O7CPQ7 salmonella |
| 39 | 36 | 63.2 | 301 | 2 | 07Q4C0 | O7Q4C0 anophelis g |
| 40 | 36 | 63.2 | 307 | 2 | 08LAW9 | O8LAW9 arabidopsis |
| 41 | 36 | 63.2 | 307 | 2 | 067ZM1 | O67ZM1 arabidopsis |
| 42 | 36 | 63.2 | 307 | 2 | 067ZM1 | O67ZM1 arabidopsis |
| 43 | 36 | 63.2 | 337 | 1 | Y8Z1_YEAST | P38278 saccharomyc |
| 44 | 36 | 63.2 | 349 | 2 | 09SRT5 | O9SRT5 arabidopsis |
| 45 | 36 | 63.2 | 379 | 2 | 0948E9 | O948E9 oryza sativ |

ALIGNMENTS

RESULT 1
TF3B_SCHPO STANDARD; PRT; 500 AA.
AC O9P6R0; O9USU4;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Transcription factor IIB 60 kDa subunit (TFIIB) (B-related factor)
DE (BRF) (TFIIB-related factor).
GN Name=Brf1; ORFNames=SPBC13E7.10C, SPBC0D10.20;
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Baeham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Felwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinovitch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volkart G., Aert R., Robben J., Gymnopoulos B.,
RA Wellens J., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moesli D., Hilbert H.,
RA Borym K., Langer I., Beck A., Leinrich E., Moesli D., Hilbert H.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Leleau V., Motier S.,
RA Gallbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Rhode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Centi L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shepkovskii G.V., Ussery D., Barrell B.G., Nuree P.,
RT "The genome sequence of Schizosaccharomyces pombe."
RL Nature 415:871-880(2002).
RN [2]
RP INTERACTION WITH TBP.
RX MEDLINE=22569152; PubMed=12682361; DOI=10.1093/nar/gkx301;
RA Huang Y., McGillicuddy E., Weinid M., Dong S., Maria R.J.,
RT "The fission yeast TFIIB-related factor limits RNA polymerase III to a
RT TATA-dependent pathway of TBP recruitment."
RL Nucleic Acids Res. 31:2108-2116(2003).
CC -1- FUNCTION: General activator of RNA polymerase III transcription.
-1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 2, 2005, 13:03:56 ; Search time 32.648 Seconds

(without alignments)
122.435 Million cell updates/sec

Title: US-09-642-744D-17

Perfect score: 57

Sequence: 1 RRIIRKIHNIK 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1426032 seqs, 333106140 residues

Total number of hits satisfying chosen parameters: 1426032

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

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- 3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep.*
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- 14: /cgn2_6/ptodata/1/pubppaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubppaa/US10C_PUBCOMB.pep.*
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- 17: /cgn2_6/ptodata/1/pubppaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubppaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 2 | 57 | 100.0 | 14 | US-10-060-102-18 | Sequence 18, Appl |
| 3 | 57 | 100.0 | 14 | US-10-060-102-19 | Sequence 19, Appl |
| 4 | 57 | 100.0 | 14 | US-10-060-102-20 | Sequence 20, Appl |
| 5 | 57 | 100.0 | 14 | US-10-721-839-13 | Sequence 13, Appl |
| 6 | 57 | 100.0 | 14 | US-10-721-839-18 | Sequence 18, Appl |
| 7 | 57 | 100.0 | 14 | US-10-721-839-19 | Sequence 19, Appl |
| 8 | 57 | 100.0 | 14 | US-10-721-839-20 | Sequence 20, Appl |
| 9 | 57 | 100.0 | 16 | US-10-060-102-14 | Sequence 14, Appl |
| 10 | 57 | 100.0 | 16 | US-10-060-102-15 | Sequence 15, Appl |
| 11 | 57 | 100.0 | 16 | US-10-721-839-14 | Sequence 14, Appl |
| 12 | 57 | 100.0 | 16 | US-10-721-839-15 | Sequence 15, Appl |
| 13 | 57 | 100.0 | 18 | US-09-840-009-2 | Sequence 2, Appl |

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| 14 | 57 | 100.0 | 18 | 9 | US-09-840-009-9 | Sequence 9, Appl |
| 15 | 57 | 100.0 | 18 | 9 | US-09-840-009-16 | Sequence 16, Appl |
| 16 | 57 | 100.0 | 18 | 9 | US-09-840-009-23 | Sequence 23, Appl |
| 17 | 57 | 100.0 | 18 | 9 | US-09-840-009-30 | Sequence 30, Appl |
| 18 | 57 | 100.0 | 18 | 14 | US-10-060-102-9 | Sequence 9, Appl |
| 19 | 57 | 100.0 | 18 | 14 | US-10-060-102-10 | Sequence 10, Appl |
| 20 | 57 | 100.0 | 18 | 14 | US-10-060-102-11 | Sequence 11, Appl |
| 21 | 57 | 100.0 | 18 | 14 | US-10-060-102-12 | Sequence 12, Appl |
| 22 | 57 | 100.0 | 18 | 15 | US-10-721-839-9 | Sequence 9, Appl |
| 23 | 57 | 100.0 | 18 | 15 | US-10-721-839-10 | Sequence 10, Appl |
| 24 | 57 | 100.0 | 18 | 15 | US-10-721-839-11 | Sequence 11, Appl |
| 25 | 57 | 100.0 | 18 | 15 | US-10-721-839-12 | Sequence 12, Appl |
| 26 | 57 | 100.0 | 29 | 15 | US-10-060-102-8 | Sequence 8, Appl |
| 27 | 57 | 100.0 | 29 | 15 | US-10-721-839-8 | Sequence 8, Appl |
| 28 | 52 | 91.2 | 18 | 9 | US-09-840-009-4 | Sequence 4, Appl |
| 29 | 52 | 91.2 | 18 | 9 | US-09-840-009-8 | Sequence 8, Appl |
| 30 | 52 | 91.2 | 18 | 9 | US-09-840-009-11 | Sequence 11, Appl |
| 31 | 52 | 91.2 | 18 | 9 | US-09-840-009-15 | Sequence 15, Appl |
| 32 | 52 | 91.2 | 18 | 9 | US-09-840-009-18 | Sequence 18, Appl |
| 33 | 52 | 91.2 | 18 | 9 | US-09-840-009-22 | Sequence 22, Appl |
| 34 | 52 | 91.2 | 18 | 9 | US-09-840-009-25 | Sequence 25, Appl |
| 35 | 52 | 91.2 | 18 | 9 | US-09-840-009-29 | Sequence 29, Appl |
| 36 | 52 | 91.2 | 18 | 14 | US-10-060-102-25 | Sequence 25, Appl |
| 37 | 52 | 91.2 | 18 | 15 | US-10-721-839-25 | Sequence 25, Appl |
| 38 | 51 | 89.5 | 18 | 9 | US-09-840-009-5 | Sequence 5, Appl |
| 39 | 51 | 89.5 | 18 | 9 | US-09-840-009-12 | Sequence 12, Appl |
| 40 | 51 | 89.5 | 18 | 9 | US-09-840-009-19 | Sequence 19, Appl |
| 41 | 51 | 89.5 | 18 | 9 | US-09-840-009-26 | Sequence 26, Appl |
| 42 | 50 | 87.7 | 18 | 9 | US-09-840-009-6 | Sequence 6, Appl |
| 43 | 50 | 87.7 | 18 | 9 | US-09-840-009-7 | Sequence 7, Appl |
| 44 | 50 | 87.7 | 18 | 9 | US-09-840-009-13 | Sequence 13, Appl |
| 45 | 50 | 87.7 | 18 | 9 | US-09-840-009-14 | Sequence 14, Appl |

ALIGNMENTS

RESULT 1
US-10-060-102-13
Sequence 13, Application US/10060102
Publication No. US20030022829A1
GENERAL INFORMATION:
APPLICANT: MAURY, WENDY
APPLICANT: STAPLETON, JACK
APPLICANT: ROLLER, RICHARD
APPLICANT: STINSKI, MARK
APPLICANT: MCCRAY, PAUL B.
TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMAL
FILE REFERENCE: IOWA:035US
CURRENT APPLICATION NUMBER: US/10/060,102
CURRENT FILING DATE: 2002-02-22
PRIOR APPLICATION NUMBER: 60/309,368
PRIOR FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/265,270
PRIOR FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-060-102-13

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Best Local Similarity 100.0%; Pred. No. 0.0045;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OR 1 RRIIRKIHNIK 12

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:18:40 ; Search time 11.3966 Seconds

(without alignments)
78.601 Million cell updates/sec

Title: US-09-642-744D-17

Perfect score: 57

Sequence: 1 RRIIRKIHNIK 12

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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4: /cgn2_6/prodata/1/aa/6B.COMB.pep.*
5: /cgn2_6/prodata/1/aa/PTUS.COMB.pep.*
6: /cgn2_6/prodata/1/aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|------------------|
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| 2 | 57 | 100.0 | 18 | 4 | US-09-840-009-9 |
| 3 | 57 | 100.0 | 18 | 4 | US-09-840-009-16 |
| 4 | 57 | 100.0 | 18 | 4 | US-09-840-009-23 |
| 5 | 57 | 100.0 | 18 | 4 | US-09-840-009-30 |
| 6 | 52 | 91.2 | 18 | 4 | US-09-840-009-4 |
| 7 | 52 | 91.2 | 18 | 4 | US-09-840-009-8 |
| 8 | 52 | 91.2 | 18 | 4 | US-09-840-009-11 |
| 9 | 52 | 91.2 | 18 | 4 | US-09-840-009-15 |
| 10 | 52 | 91.2 | 18 | 4 | US-09-840-009-18 |
| 11 | 52 | 91.2 | 18 | 4 | US-09-840-009-22 |
| 12 | 52 | 91.2 | 18 | 4 | US-09-840-009-25 |
| 13 | 52 | 91.2 | 18 | 4 | US-09-840-009-29 |
| 14 | 51 | 89.5 | 18 | 4 | US-09-840-009-5 |
| 15 | 51 | 89.5 | 18 | 4 | US-09-840-009-12 |
| 16 | 51 | 89.5 | 18 | 4 | US-09-840-009-19 |
| 17 | 51 | 89.5 | 18 | 4 | US-09-840-009-26 |
| 18 | 50 | 87.7 | 18 | 4 | US-09-840-009-6 |
| 19 | 50 | 87.7 | 18 | 4 | US-09-840-009-7 |
| 20 | 50 | 87.7 | 18 | 4 | US-09-840-009-13 |
| 21 | 50 | 87.7 | 18 | 4 | US-09-840-009-14 |
| 22 | 50 | 87.7 | 18 | 4 | US-09-840-009-20 |
| 23 | 50 | 87.7 | 18 | 4 | US-09-840-009-21 |
| 24 | 50 | 87.7 | 18 | 4 | US-09-840-009-27 |
| 25 | 50 | 87.7 | 18 | 4 | US-09-840-009-28 |
| 26 | 49 | 86.0 | 18 | 4 | US-09-840-009-3 |
| 27 | 49 | 86.0 | 18 | 4 | US-09-840-009-10 |

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| 28 | 49 | 86.0 | 18 | 4 | US-09-840-009-17 | Sequence 17, Appl |
| 29 | 49 | 86.0 | 18 | 4 | US-09-840-009-24 | Sequence 24, Appl |
| 30 | 49 | 86.0 | 18 | 4 | US-09-840-009-31 | Sequence 31, Appl |
| 31 | 49 | 86.0 | 18 | 4 | US-09-840-009-34 | Sequence 34, Appl |
| 32 | 49 | 86.0 | 18 | 4 | US-09-840-009-35 | Sequence 35, Appl |
| 33 | 41 | 71.9 | 18 | 4 | US-09-840-009-32 | Sequence 32, Appl |
| 34 | 41 | 71.9 | 18 | 4 | US-09-840-009-33 | Sequence 33, Appl |
| 35 | 41 | 71.9 | 18 | 4 | US-09-840-009-36 | Sequence 36, Appl |
| 36 | 41 | 71.9 | 18 | 4 | US-09-840-009-37 | Sequence 37, Appl |
| 37 | 37 | 64.9 | 18 | 4 | US-09-840-009-1 | Sequence 1, Appl |
| 38 | 37 | 64.9 | 18 | 4 | US-09-840-009-3 | Sequence 3, Appl |
| 39 | 37 | 64.9 | 18 | 4 | US-09-840-009-5 | Sequence 5, Appl |
| 40 | 37 | 64.9 | 18 | 4 | US-09-840-009-6 | Sequence 6, Appl |
| 41 | 37 | 64.9 | 18 | 4 | US-09-840-009-7 | Sequence 7, Appl |
| 42 | 37 | 64.9 | 18 | 4 | US-09-840-009-8 | Sequence 8, Appl |
| 43 | 37 | 64.9 | 18 | 4 | US-09-840-009-9 | Sequence 9, Appl |
| 44 | 36 | 63.2 | 18 | 4 | US-09-840-009-10 | Sequence 10, Appl |
| 45 | 36 | 63.2 | 18 | 4 | US-09-840-009-11 | Sequence 11, Appl |

ALIGNMENTS

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RESULT 1
US-09-840-009-2
Sequence 2, Application US/09840009
Patent No. 6492328
GENERAL INFORMATION:
APPLICANT: Lehner, Robert I.
APPLICANT: Tack, Brian F.
TITLE OF INVENTION: NOVIISPRINS: ANTIMICROBIAL PEPTIDES
FILE REFERENCE: 06510-195W0
CURRENT APPLICATION NUMBER: US/09/840,009
PRIOR FILING DATE: 2001-04-19
PRIOR APPLICATION NUMBER: US 09/606,858
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic antimicrobial peptide
US-09-840-009-2
Query Match
Best Local Similarity 100.0%; Score 57; DB 4; Length 18;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RRIIRKIHNIK 12
DB 4 RRIIRKIHNIK 15
RESULT 2
US-09-840-009-9
Sequence 9, Application US/09840009
Patent No. 6492328
GENERAL INFORMATION:
APPLICANT: Lehner, Robert I.
APPLICANT: Tack, Brian F.
TITLE OF INVENTION: NOVIISPRINS: ANTIMICROBIAL PEPTIDES
FILE REFERENCE: 06510-195W0
CURRENT APPLICATION NUMBER: US/09/840,009
PRIOR FILING DATE: 2001-04-19
PRIOR APPLICATION NUMBER: US 09/606,858
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:17:55 ; Search time 42.067 Seconds
(without alignments)
110.327 Million cell updates/sec

Title: US-09-642-744D-17

Perfect score: 57

Sequence: 1 RRIIRKIHNIK 12

Scoring table: BLOSUM62
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Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: geneseqp20008:*
4: geneseqp20018:*
5: geneseqp20028:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 3 | 57 | 100.0 | 13 | 4 AAB70663 | Aab70663 Ovine SMA |
| 4 | 57 | 100.0 | 14 | 4 AAB70658 | Aab70658 Ovine SMA |
| 5 | 57 | 100.0 | 14 | 4 AAB70659 | Aab70659 Ovine SMA |
| 6 | 57 | 100.0 | 14 | 4 AAB70661 | Aab70661 Ovine SMA |
| 7 | 57 | 100.0 | 14 | 4 AAB70660 | Aab70660 Ovine SMA |
| 8 | 57 | 100.0 | 14 | 5 AAB70662 | Aab70662 Ovine SMA |
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| 10 | 57 | 100.0 | 14 | 5 AAB70662 | Aab70662 Ovine SMA |
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| 16 | 57 | 100.0 | 16 | 4 AAB70660 | Aab70660 Ovine SMA |
| 17 | 57 | 100.0 | 18 | 4 AAB70664 | Aab70664 Ovine SMA |
| 18 | 57 | 100.0 | 18 | 4 AAB70665 | Aab70665 Ovine SMA |
| 19 | 57 | 100.0 | 18 | 5 AAB70662 | Aab70662 Ovine SMA |
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| 23 | 57 | 100.0 | 18 | 5 AAB70666 | Aab70666 Ovine SMA |
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| 25 | 57 | 100.0 | 18 | 5 AAB70668 | Aab70668 Ovine SMA |

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| 27 | 57 | 100.0 | 18 | 5 AAB70665 | Aab70665 Ovine SMA |
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| 39 | 57 | 100.0 | 29 | 5 AAB70665 | Aab70665 Ovine SMA |
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| 41 | 57 | 100.0 | 29 | 5 AAB70665 | Aab70665 Ovine SMA |
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| 43 | 57 | 100.0 | 29 | 5 AAB70665 | Aab70665 Ovine SMA |
| 44 | 57 | 100.0 | 29 | 5 AAB70665 | Aab70665 Ovine SMA |
| 45 | 57 | 100.0 | 29 | 5 AAB70665 | Aab70665 Ovine SMA |

ALIGNMENTS

RESULT 1

AAB70664 standard; peptide; 12 AA.

AAB70664;

15-MAY-2001 (first entry)

Ovine SNAP 29 cathelicidin derived antimicrobial peptide SEQ ID NO:17.

Ovine: SNAP29; lupine: RCAP 18; cathelicidin; antimicrobial;

bactericidal; antibiotic; antiviral; microbial growth inhibitor;

proliferation inhibitor; gene therapy; Pseudomonas aeruginosa;

Burkholderia cepacia; Alcaligenes; Xanthomonas.

Ovis aries.

WO200112668-A1.

22-FEB-2001.

18-AUG-2000; 2000WO-US022781.

18-AUG-1999; 99US-0149886P.

(IOWA) UNIV IOWA RES FOUND.

(REGC) UNIV CALIFORNIA.

Tack BE, Mccrory P, Welsh M, Travis SM, Lehrer R;

WPI; 2001-234911/24.

New antimicrobial peptides useful as antibiotics for inhibiting growth

and proliferation of microbes, and for treating microbial infections.

Claim 1; Page 103; 137pp; English.

AAB70668 to AAB70675 represent antimicrobial peptides (1), of which SNAP 29 cathelicidin family peptide, and AAB70665 to AAB70673 are derived from the lupine RCAP 18 cathelicidin family peptide, and can be used as antimicrobial and antiviral activities, and can be used as microbial growth and proliferation inhibitors and in gene therapy. (1) are useful for inhibiting microbial growth in an environment capable of sustaining such growth, for inhibiting microbial growth or strain in a host, and inhibiting the growth of drug-resistant microbial strains such as Pseudomonas aeruginosa, Burkholderia cepacia, Alcaligenes and Xanthomonas

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:17:06 ; Search time 40.5615 Seconds
(without alignments)
164.122 Million cell updates/sec

Title: US-09-642-744d-16
Perfect score: 62
Sequence: 1 RRIKRIHIKK 13

Scoring table:

BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 43 | 69.4 | 638 | 2 | Q8D796 |
| 2 | 43 | 69.4 | 660 | 2 | Q7MEAO |
| 3 | 42 | 67.7 | 125 | 2 | Q9AVZ1 |
| 4 | 42 | 67.7 | 308 | 2 | Q8R2C7 |
| 5 | 42 | 67.7 | 500 | 1 | TF3B_SCHPO |
| 6 | 41 | 66.1 | 337 | 1 | YB21_YEAST |
| 7 | 41 | 66.1 | 414 | 2 | Q947U2 |
| 8 | 41 | 66.1 | 613 | 1 | Q7XEY8 |
| 9 | 41 | 66.1 | 613 | 1 | DEAD_HAETN |
| 10 | 41 | 66.1 | 670 | 1 | REP_BUCBP |
| 11 | 40 | 64.5 | 256 | 2 | Q83CP2 |
| 12 | 40 | 64.5 | 370 | 2 | O67743 |
| 13 | 40 | 64.5 | 452 | 2 | Q7N787 |
| 14 | 40 | 64.5 | 475 | 2 | Q7SG18 |
| 15 | 39 | 62.9 | 202 | 1 | HAM1_AQUAE |
| 16 | 39 | 62.9 | 210 | 2 | Q92C15 |
| 17 | 39 | 62.9 | 250 | 2 | Q7W5F0 |
| 18 | 39 | 62.9 | 250 | 2 | Q7W5F0 |
| 19 | 39 | 62.9 | 258 | 2 | Q8MY71 |
| 20 | 39 | 62.9 | 407 | 2 | Q9UTH1 |
| 21 | 39 | 62.9 | 461 | 2 | Q81BM2 |
| 22 | 39 | 62.9 | 483 | 2 | Q9KR81 |
| 23 | 39 | 62.9 | 598 | 2 | Q7VTH0 |
| 24 | 39 | 62.9 | 967 | 2 | Q7RJ84 |
| 25 | 39 | 62.9 | 1157 | 2 | Q7R0N5 |
| 26 | 39 | 62.9 | 1157 | 2 | Q7R0N5 |
| 27 | 39 | 62.9 | 4057 | 2 | Q81J57 |
| 28 | 38 | 61.3 | 87 | 1 | SSS1_SCYCA |
| 29 | 38 | 61.3 | 160 | 1 | SCS1_SHEEP |
| 30 | 38 | 61.3 | 160 | 1 | SCS2_SHEEP |
| 31 | 38 | 61.3 | 262 | 2 | Q720G5 |

| | | | | | |
|----|----|------|-----|---|------------|
| 32 | 38 | 61.3 | 272 | 2 | Q8YFUG |
| 33 | 38 | 61.3 | 415 | 2 | Q9SPU4 |
| 34 | 38 | 61.3 | 428 | 2 | Q8TXS5 |
| 35 | 38 | 61.3 | 457 | 1 | BAG4_HUMAN |
| 36 | 38 | 61.3 | 457 | 1 | BAG4_MOUSE |
| 37 | 38 | 61.3 | 491 | 2 | Q9H8X2 |
| 38 | 38 | 61.3 | 574 | 2 | SYP_BUCBP |
| 39 | 38 | 61.3 | 623 | 1 | Y014_MYCPN |
| 40 | 38 | 61.3 | 636 | 2 | Q87HT7 |
| 41 | 38 | 61.3 | 670 | 1 | REP_HAETN |
| 42 | 38 | 61.3 | 834 | 2 | Q7RR10 |
| 43 | 38 | 61.3 | 878 | 2 | Q7RY40 |
| 44 | 37 | 59.7 | 41 | 2 | Q48971 |
| 45 | 37 | 59.7 | 207 | 2 | Q846Q4 |

ALIGNMENTS

RESULT 1

| | | | | |
|-----------------------|---|---------------|-----------|-------------|
| ID | Q8D796 | PRELIMINARY; | PRT; | 638 AA. |
| AC | Q8D796; | | | |
| DT | 01-MAR-2003 (T-EMBLrel. 23, Created) | | | |
| DT | 01-MAR-2003 (T-EMBLrel. 23, Last sequence update) | | | |
| DT | 01-MAR-2004 (T-EMBLrel. 26, Last annotation update) | | | |
| DE | Predicted signal transduction protein. | | | |
| GN | OrderedLocustNames=V20264; | | | |
| OS | Vibrio vulnificus. | | | |
| OC | Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; | | | |
| OC | Vibrionaceae; Vibrrio. | | | |
| OX | NCBI_Taxid=672; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | STRAIN=CMCP6; | | | |
| RA | Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H., | | | |
| RA | Choy H.E.; | | | |
| RT | *Complete genome sequence of Vibrio vulnificus CMCP6.; | | | |
| RL | Submitted (DEC-2002) to the EMBL/Genbank/DBJ databases. | | | |
| DR | EMBL; AB016808; AA007230.1; - | | | |
| DR | InterPro; IPR001633; EAL. | | | |
| DR | InterPro; IPR003018; GAF. | | | |
| DR | InterPro; IPR000160; GGDEF. | | | |
| DR | Pfam; PF00563; EAL; 1. | | | |
| DR | Pfam; PF00590; GAF; 1. | | | |
| DR | Pfam; PF00990; GGDEF; 1. | | | |
| DR | SMART; SM00052; DUF2; 1. | | | |
| DR | SMART; SM00065; GAF; 1. | | | |
| DR | TIGRFAMs; TIGR00254; GGDEF; 1. | | | |
| DR | PROSITE; PS00883; EAL; 1. | | | |
| DR | PROSITE; PS00887; GGDEF; 1. | | | |
| KW | Complete proteome. | | | |
| SQ | SEQUENCE 638 AA; 72187 MW; 7D13E28DF3A3F099 CRC64; | | | |
| Qy | 1 RRIKRIHIKK 13 | | | |
| Db | 566 KEIRSIHIHAKK 578 | | | |
| Query Match | 69.4%; | Score 43; | DB 2; | Length 638; |
| Best Local Similarity | 61.5%; | Pred. No. 41; | | |
| Matches | 8; Conservative | 2; Mismatches | 3; Indels | 0; Gaps 0; |
| RESULT 2 | | | | |
| ID | Q7MEAO | PRELIMINARY; | PRT; | 660 AA. |
| AC | Q7MEAO; | | | |
| DT | 01-MAR-2004 (T-EMBLrel. 26, Created) | | | |
| DT | 01-MAR-2004 (T-EMBLrel. 26, Last sequence update) | | | |
| DT | 01-MAR-2004 (T-EMBLrel. 26, Last annotation update) | | | |
| DE | GGDEF family protein. | | | |
| GN | OrderedLocustNames=VVA0770; | | | |
| OS | Vibrio vulnificus (strain Y016). | | | |

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:21:40 ; Search time 8.06145 Seconds

(without alignment)
155.160 Million cell updates/sec

Title: US-09-642-744D-16

Perfect score: 62

Sequence: 1 RRIIRKIIHIKK 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.79:.*
2: PIR2:.*
3: PIR3:.*
4: PIR4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|---------------------|
| 1 | 42 | 67.7 | 125 | 2 A99114 | hypothetical prote |
| 2 | 41 | 66.1 | 137 | 2 S46010 | hypothetical prote |
| 3 | 41 | 66.1 | 613 | 2 F64056 | probable ATP-depen |
| 4 | 40 | 64.5 | 370 | 2 C70464 | GTP-binding protei |
| 5 | 39 | 62.9 | 202 | 1 H70318 | conserved hypochet |
| 6 | 39 | 62.9 | 210 | 2 AC1577 | precortin isomeras |
| 7 | 39 | 62.9 | 407 | 2 T37688 | hypothetical prote |
| 8 | 39 | 62.9 | 483 | 2 B82160 | hypothetical prote |
| 9 | 39 | 62.9 | 867 | 2 G69485 | DNA-directed RNA p |
| 10 | 38 | 61.3 | 87 | 2 S00180 | spermatid protein |
| 11 | 38 | 61.3 | 152 | 2 S68411 | cathecin-related p |
| 12 | 38 | 61.3 | 160 | 2 S68412 | myeloid antimicrob |
| 13 | 38 | 61.3 | 150 | 2 S68228 | transposase BME114 |
| 14 | 38 | 61.3 | 272 | 2 AB3430 | transposase BME114 |
| 15 | 38 | 61.3 | 623 | 2 S73462 | transposase BME114 |
| 16 | 38 | 61.3 | 698 | 2 D64084 | helicase (RC 3.6.1 |
| 17 | 37 | 59.7 | 41 | 2 S77768 | hypothetical prote |
| 18 | 37 | 59.7 | 334 | 2 B72301 | endoglucanase - Th |
| 19 | 37 | 59.7 | 368 | 2 C69884 | conserved hypochet |
| 20 | 37 | 59.7 | 559 | 2 C83952 | prolyl-tRNA synthet |
| 21 | 36 | 58.1 | 117 | 2 T12722 | hypothetical prote |
| 22 | 36 | 58.1 | 284 | 2 A10897 | tagatase-bisphosph |
| 23 | 36 | 58.1 | 299 | 2 G72307 | hypothetical prote |
| 24 | 36 | 58.1 | 310 | 2 A33489 | hypothetical prote |
| 25 | 36 | 58.1 | 370 | 2 A05034 | hypothetical prote |
| 26 | 36 | 58.1 | 447 | 2 P81678 | GTP-binding protei |
| 27 | 36 | 58.1 | 499 | 2 G84972 | leucyl aminopeptid |
| 28 | 36 | 58.1 | 627 | 2 C82418 | GGDPF family prote |
| 29 | 36 | 58.1 | 760 | 2 T24521 | hypothetical prote |

| | | | | | |
|----|----|------|-----|----------|--------------------|
| 30 | 35 | 56.5 | 128 | 2 A12766 | transcription regu |
| 31 | 35 | 56.5 | 128 | 2 D97547 | probable transcrip |
| 32 | 35 | 56.5 | 164 | 2 T50602 | ribosomal protein |
| 33 | 35 | 56.5 | 164 | 2 G86230 | hypothetical prote |
| 34 | 35 | 56.5 | 164 | 2 H96610 | hypothetical prote |
| 35 | 35 | 56.5 | 212 | 2 A64045 | probable 60S ribos |
| 36 | 35 | 56.5 | 220 | 2 C53376 | 2-dehydro-3-deoxy- |
| 37 | 35 | 56.5 | 222 | 2 F72572 | hypothetical prote |
| 38 | 35 | 56.5 | 330 | 2 T22852 | probable TAPA-box |
| 39 | 35 | 56.5 | 381 | 2 F71078 | hypothetical prote |
| 40 | 35 | 56.5 | 414 | 2 G71331 | hypothetical prote |
| 41 | 35 | 56.5 | 420 | 2 E72357 | probable cell divi |
| 42 | 35 | 56.5 | 420 | 2 S45630 | sugar ABC transpor |
| 43 | 35 | 56.5 | 436 | 2 G97186 | DNA primase chain |
| 44 | 35 | 56.5 | 491 | 2 AC1185 | diverged glycosylc |
| 45 | 35 | 56.5 | 494 | 2 AB1543 | B. subtilis YDB p |

ALIGNMENTS

RESULT 1

A99114
hypothetical protein orf125 [imported] - Guillardia theta nucleomorph
C/Species: nucleomorph Guillardia theta
A/Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #ext_change 09-Jul-2004
C/Accession: A99114
R/Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Re
Nature 410, 1091-1096, 2001
A/Title: The highly reduced genome of an enslaved algal nucleus.
A/Reference number: A99082; MUID:11323671; PMID:11323671
A/Accession: A99114
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-125 <DOU>
A/Cross-references: UNIPROT:Q9AVZ1; GB:AJ010592; NID:G12580762; PIDN:CAC27080.1; GSPDB:
C/Genetics:
A/Gen: orf125
A/Map position: 2
A/Genome: nucleomorph
C/Keywords: nucleomorph

Query Match 67.7%; Score 42; DB 2; Length 125;
Best Local Similarity 70.0%; Pred. No. 4.4;

Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 IRKIIHIKK 13
|||||:
Db 9 IRKIIHLVRK 18

RESULT 2

S46010
hypothetical protein YBR141c - Yeast (Saccharomyces cerevisiae)

N/Alternate names: hypothetical protein YBR1118

C/Species: Saccharomyces cerevisiae

C/Date: 26-Aug-1994 #sequence_revision 09-Sep-1994 #ext_change 09-Jul-2004

C/Accession: S46010

R/Becam, A.M.; Herbert, C.J.; Nasr, F.; Slonimski, P.P.; Zagulski, M.

submitted to the Protein Sequence Database, August 1994

A/Reference number: S45995

A/Accession: S46010

A/Molecule type: DNA

A/Residues: 1-337 <BEC>

A/Cross-references: UNIPROT:P38278; EMBL:Z36010; NID:G536439; PID:G536440; GSPDB:GN0000

A/Experimental source: strain S288C

C/Genetics:

A/Gen: MIPS:YBR141c

A/Cross-references: SGD:S0000345

A/Map position: 2R

Query Match 66.1%; Score 41; DB 2; Length 337;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:18:40 ; Search time 12.3464 Seconds

(without alignments)
78.601 Million cell updates/sec

Title: US-09-642-744D-16

Perfect score: 62

Sequence: 1 RRIIRKIHIIKK 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PTUS.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|------------------|
| 1 | 62 | 100.0 | 18 | 4 | US-09-840-009-2 |
| 2 | 62 | 100.0 | 18 | 4 | US-09-840-009-9 |
| 3 | 62 | 100.0 | 18 | 4 | US-09-840-009-16 |
| 4 | 62 | 100.0 | 18 | 4 | US-09-840-009-23 |
| 5 | 62 | 100.0 | 18 | 4 | US-09-840-009-30 |
| 6 | 57 | 91.9 | 18 | 4 | US-09-840-009-4 |
| 7 | 57 | 91.9 | 18 | 4 | US-09-840-009-8 |
| 8 | 57 | 91.9 | 18 | 4 | US-09-840-009-11 |
| 9 | 57 | 91.9 | 18 | 4 | US-09-840-009-15 |
| 10 | 57 | 91.9 | 18 | 4 | US-09-840-009-18 |
| 11 | 57 | 91.9 | 18 | 4 | US-09-840-009-22 |
| 12 | 57 | 91.9 | 18 | 4 | US-09-840-009-25 |
| 13 | 57 | 91.9 | 18 | 4 | US-09-840-009-29 |
| 14 | 56 | 90.3 | 18 | 4 | US-09-840-009-5 |
| 15 | 56 | 90.3 | 18 | 4 | US-09-840-009-12 |
| 16 | 56 | 90.3 | 18 | 4 | US-09-840-009-19 |
| 17 | 56 | 90.3 | 18 | 4 | US-09-840-009-26 |
| 18 | 55 | 88.7 | 18 | 4 | US-09-840-009-6 |
| 19 | 55 | 88.7 | 18 | 4 | US-09-840-009-7 |
| 20 | 55 | 88.7 | 18 | 4 | US-09-840-009-13 |
| 21 | 55 | 88.7 | 18 | 4 | US-09-840-009-14 |
| 22 | 55 | 88.7 | 18 | 4 | US-09-840-009-20 |
| 23 | 55 | 88.7 | 18 | 4 | US-09-840-009-21 |
| 24 | 55 | 88.7 | 18 | 4 | US-09-840-009-27 |
| 25 | 55 | 88.7 | 18 | 4 | US-09-840-009-28 |
| 26 | 54 | 87.1 | 18 | 4 | US-09-840-009-3 |
| 27 | 54 | 87.1 | 18 | 4 | US-09-840-009-10 |

| | | | | | | |
|----|----|------|-----|---|-------------------|--------------------|
| 28 | 54 | 87.1 | 18 | 4 | US-09-840-009-17 | Sequence 17, Appl |
| 29 | 54 | 87.1 | 18 | 4 | US-09-840-009-24 | Sequence 24, Appl |
| 30 | 54 | 87.1 | 18 | 4 | US-09-840-009-31 | Sequence 31, Appl |
| 31 | 54 | 87.1 | 18 | 4 | US-09-840-009-34 | Sequence 34, Appl |
| 32 | 54 | 87.1 | 18 | 4 | US-09-840-009-35 | Sequence 35, Appl |
| 33 | 46 | 74.2 | 18 | 4 | US-09-840-009-32 | Sequence 32, Appl |
| 34 | 46 | 74.2 | 18 | 4 | US-09-840-009-33 | Sequence 33, Appl |
| 35 | 46 | 74.2 | 18 | 4 | US-09-840-009-36 | Sequence 36, Appl |
| 36 | 46 | 74.2 | 18 | 4 | US-09-840-009-37 | Sequence 37, Appl |
| 37 | 42 | 67.7 | 18 | 4 | US-09-840-009-1 | Sequence 1, Appl |
| 38 | 41 | 66.1 | 337 | 4 | US-09-538-092-38 | Sequence 38, Appl |
| 39 | 39 | 62.9 | 24 | 4 | US-09-785-0598-5 | Sequence 5, Appl |
| 40 | 39 | 62.9 | 36 | 4 | US-09-785-0598-6 | Sequence 6, Appl |
| 41 | 39 | 62.9 | 42 | 4 | US-09-785-0598-7 | Sequence 7, Appl |
| 42 | 39 | 62.9 | 48 | 4 | US-09-785-0598-8 | Sequence 8, Appl |
| 43 | 38 | 61.3 | 149 | 4 | US-09-774-639-304 | Sequence 104, Appl |
| 44 | 38 | 61.3 | 160 | 4 | US-09-917-340-36 | Sequence 36, Appl |
| 45 | 38 | 61.3 | 229 | 4 | US-09-394-1428-8 | Sequence 8, Appl |

ALIGNMENTS

```
RESULT 1
US-09-840-009-2
Sequence 2, Application US/09840009
Patent No. 6492328
GENERAL INFORMATION:
APPLICANT: Lehner, Robert I.
APPLICANT: Waring, Robert J.
APPLICANT: Tack, Brian F.
TITLE OF INVENTION: NOVISPIRINS: ANTIMICROBIAL PEPTIDES
FILE REFERENCE: 06510-195WO
CURRENT FILING DATE: US/09/840,009
PRIOR FILING DATE: 2001-04-19
PRIOR APPLICATION NUMBER: US 09/606,858
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic antimicrobial peptide
US-09-840-009-2
Query Match          100.0%; Score 62; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 RRIIRKIHIIKK 13
Db      4 RRIIRKIHIIKK 16
RESULT 2
US-09-840-009-9
Sequence 9, Application US/09840009
Patent No. 6492328
GENERAL INFORMATION:
APPLICANT: Lehner, Robert I.
APPLICANT: Waring, Robert J.
APPLICANT: Tack, Brian F.
TITLE OF INVENTION: NOVISPIRINS: ANTIMICROBIAL PEPTIDES
FILE REFERENCE: 06510-195WO
CURRENT FILING DATE: US/09/840,009
PRIOR FILING DATE: 2001-04-19
PRIOR APPLICATION NUMBER: US 09/606,858
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:17:55 ; Search time 45.5726 Seconds
(without alignments)
110.327 Million cell updates/sec

Title: US-09-642-744D-16
Perfect score: 62
Sequence: 1 RRIIRKIHICK 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp19808:*
2: geneseqp19908:*
3: geneseqp20008:*
4: geneseqp20018:*
5: geneseqp20028:*
6: geneseqp20038:*
7: geneseqp20048:*
8: geneseqp20058:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|------------|--------------------|
| 1 | 62 | 100.0 | 13 | 4 AAB70663 | Aab70663 Ovine SMA |
| 2 | 62 | 100.0 | 14 | 4 AAB70658 | Aab70658 Ovine SMA |
| 3 | 62 | 100.0 | 14 | 4 AAB70659 | Aab70659 Ovine SMA |
| 4 | 62 | 100.0 | 14 | 4 AAB70661 | Aab70661 Ovine SMA |
| 5 | 62 | 100.0 | 14 | 4 AAB70660 | Aab70660 Ovine SMA |
| 6 | 62 | 100.0 | 14 | 4 AAB70657 | Aab70657 Ovine SMA |
| 7 | 62 | 100.0 | 14 | 4 AAB70656 | Aab70656 Ovine SMA |
| 8 | 62 | 100.0 | 14 | 4 AAB70655 | Aab70655 Ovine SMA |
| 9 | 62 | 100.0 | 14 | 4 AAB70654 | Aab70654 Ovine SMA |
| 10 | 62 | 100.0 | 14 | 4 AAB70653 | Aab70653 Ovine SMA |
| 11 | 62 | 100.0 | 14 | 4 AAB70652 | Aab70652 Ovine SMA |
| 12 | 62 | 100.0 | 14 | 4 AAB70651 | Aab70651 Ovine SMA |
| 13 | 62 | 100.0 | 14 | 4 AAB70650 | Aab70650 Ovine SMA |
| 14 | 62 | 100.0 | 14 | 4 AAB70649 | Aab70649 Ovine SMA |
| 15 | 62 | 100.0 | 14 | 4 AAB70648 | Aab70648 Ovine SMA |
| 16 | 62 | 100.0 | 14 | 4 AAB70647 | Aab70647 Ovine SMA |
| 17 | 62 | 100.0 | 14 | 4 AAB70646 | Aab70646 Ovine SMA |
| 18 | 62 | 100.0 | 14 | 4 AAB70645 | Aab70645 Ovine SMA |
| 19 | 62 | 100.0 | 14 | 4 AAB70644 | Aab70644 Ovine SMA |
| 20 | 62 | 100.0 | 14 | 4 AAB70643 | Aab70643 Ovine SMA |
| 21 | 62 | 100.0 | 14 | 4 AAB70642 | Aab70642 Ovine SMA |
| 22 | 62 | 100.0 | 14 | 4 AAB70641 | Aab70641 Ovine SMA |
| 23 | 62 | 100.0 | 14 | 4 AAB70640 | Aab70640 Ovine SMA |
| 24 | 62 | 100.0 | 14 | 4 AAB70639 | Aab70639 Ovine SMA |
| 25 | 62 | 100.0 | 14 | 4 AAB70638 | Aab70638 Ovine SMA |

| | | | | | |
|----|----|-------|----|------------|--------------------|
| 25 | 62 | 100.0 | 20 | 4 AAB70653 | Aab70653 Ovine SMA |
| 27 | 62 | 100.0 | 29 | 4 AAB70675 | Aab70675 Ovine SMA |
| 28 | 62 | 100.0 | 29 | 4 AAB70675 | Aab70675 Ovine SMA |
| 29 | 62 | 100.0 | 29 | 4 AAB70675 | Aab70675 Ovine SMA |
| 30 | 57 | 91.9 | 12 | 4 AAB70664 | Aab70664 Ovine SMA |
| 31 | 57 | 91.9 | 13 | 4 AAB70662 | Aab70662 Ovine SMA |
| 32 | 57 | 91.9 | 18 | 5 AAB70670 | Aab70670 Ovine SMA |
| 33 | 57 | 91.9 | 18 | 5 AAB70660 | Aab70660 Ovine SMA |
| 34 | 57 | 91.9 | 18 | 5 AAB70681 | Aab70681 Ovine SMA |
| 35 | 57 | 91.9 | 18 | 5 AAB70687 | Aab70687 Ovine SMA |
| 36 | 57 | 91.9 | 18 | 5 AAB70684 | Aab70684 Ovine SMA |
| 37 | 57 | 91.9 | 18 | 5 AAB70683 | Aab70683 Ovine SMA |
| 38 | 57 | 91.9 | 18 | 5 AAB70686 | Aab70686 Ovine SMA |
| 39 | 57 | 91.9 | 18 | 5 AAB70685 | Aab70685 Ovine SMA |
| 40 | 56 | 90.3 | 18 | 5 AAB70684 | Aab70684 Ovine SMA |
| 41 | 56 | 90.3 | 18 | 5 AAB70687 | Aab70687 Ovine SMA |
| 42 | 56 | 90.3 | 18 | 5 AAB70686 | Aab70686 Ovine SMA |
| 43 | 56 | 90.3 | 18 | 5 AAB70687 | Aab70687 Ovine SMA |
| 44 | 56 | 90.3 | 18 | 5 AAB70686 | Aab70686 Ovine SMA |
| 45 | 55 | 88.7 | 18 | 5 AAB70687 | Aab70687 Ovine SMA |

ALIGNMENTS

| | | |
|----------|--|---------------------------|
| RESULT 1 | AAB70663 | standard; peptide; 13 AA. |
| ID | AAB70663 | |
| AC | AAB70663 | |
| XX | | |
| DT | 15-MAY-2001 | (first entry) |
| DE | Ovine SNAP 29 cathelicidin derived antimicrobial peptide SEQ ID NO:16. | |
| XX | | |
| KW | Ovine: SNAP29; lupine: RCAP 18; cathelicidin; antimicrobial; bactericidal; antibiotic; antiviral; microbial growth inhibitor; proliferation inhibitor; gene therapy; Pseudomonas aeruginosa; Burkholderia cepacia; Alcaligenes; Xanthomonas. | |
| KW | Burkholderia cepacia; Alcaligenes; Xanthomonas. | |
| OS | Ovis aries. | |
| XX | | |
| PN | WO200112668-A1. | |
| XX | | |
| PD | 22-FEB-2001. | |
| XX | | |
| PF | 18-AUG-2000; 2000WO-US022781. | |
| XX | | |
| PR | 18-AUG-1999; 99US-0149886P. | |
| XX | | |
| PA | (IOWA) UNIV IOWA RES FOUND. | |
| XX | | |
| PA | (REGC) UNIV CALIFORNIA. | |
| XX | | |
| PI | Tack BE, McCreary P, Welsh M, Travis SM, Lehrer R, WPI; 2001-234911/24. | |
| XX | | |
| DR | | |
| XX | | |
| PT | New antimicrobial peptides useful as antibiotics for inhibiting growth and proliferation of microbes, and for treating microbial infections. | |
| XX | | |
| PS | Claim 1; Page 103; 137pp; English. | |
| XX | | |
| CC | AAB70648 to AAB70675 represent antimicrobial peptides (I), of which SNAP 29 cathelicidin family peptide, and AAB70675 are derived from the ovine antimicrobial and antiviral activites, and can be used as microbial growth and proliferation inhibitors and in gene therapy. (I) are useful for inhibiting microbial growth in an environment capable of sustaining such growth, for inhibiting microbial growth or strain in a host, and inhibiting the growth of drug-resistant microbial strains such as Pseudomonas aeruginosa, Burkholderia cepacia, Alcaligenes and Xanthomonas | |
| XX | | |

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:17:06 ; Search time 40.5615 Seconds

(without alignments)
164.122 Million cell updates/sec

Title: US-09-642-744d-15

Perfect score: 61

Sequence: 1 LRRIRKIHNIK 13

Scoring table: BLOSUM62

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniProt_sprot.*

2: uniProt_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 42 | 68.9 | 500 | 1 | TF3B_SCHPO |
| 2 | 41 | 67.2 | 670 | 1 | REP_BUCBP |
| 3 | 40 | 65.6 | 414 | 2 | Q94702 |
| 4 | 40 | 65.6 | 414 | 2 | Q7XEX8 |
| 5 | 39 | 63.9 | 202 | 1 | HAM1_AQUAE |
| 6 | 39 | 63.9 | 210 | 2 | Q92C15 |
| 7 | 39 | 63.9 | 4057 | 2 | 081UE7 |
| 8 | 38 | 62.3 | 250 | 2 | Q7W5F0 |
| 9 | 38 | 62.3 | 250 | 2 | Q7W5F0 |
| 10 | 38 | 62.3 | 262 | 2 | Q7Z0C5 |
| 11 | 38 | 62.3 | 272 | 2 | 08YFV6 |
| 12 | 38 | 62.3 | 284 | 2 | 08XGZ9 |
| 13 | 38 | 62.3 | 284 | 2 | 07CR07 |
| 14 | 38 | 62.3 | 428 | 2 | 08TXS5 |
| 15 | 38 | 62.3 | 475 | 1 | GATB_THETN |
| 16 | 38 | 62.3 | 475 | 1 | GATB_THETN |
| 17 | 38 | 62.3 | 574 | 1 | SYP_BUCBP |
| 18 | 38 | 62.3 | 598 | 2 | Q7VTH0 |
| 19 | 38 | 62.3 | 633 | 1 | Y014_MYCPN |
| 20 | 38 | 62.3 | 638 | 2 | 08D796 |
| 21 | 38 | 62.3 | 660 | 2 | Q7MEAO |
| 22 | 38 | 62.3 | 684 | 2 | 08Q0U6 |
| 23 | 38 | 62.3 | 684 | 2 | 08Q0U6 |
| 24 | 38 | 62.3 | 780 | 2 | 09DVU4 |
| 25 | 38 | 62.3 | 838 | 2 | 08AUB9 |
| 26 | 38 | 62.3 | 862 | 2 | 08AUB9 |
| 27 | 38 | 62.3 | 878 | 2 | Q7RY40 |
| 28 | 38 | 62.3 | 954 | 2 | Q9GQ15 |
| 29 | 38 | 62.3 | 969 | 2 | Q9U022 |
| 30 | 38 | 62.3 | 1157 | 2 | Q7R0N5 |
| 31 | 38 | 62.3 | 1188 | 2 | 057849 |

| | | | | | | |
|----|----|------|-----|---|------------|--------------------|
| 32 | 37 | 60.7 | 87 | 1 | SSS1_SCYCA | P13275 scyllorhinu |
| 33 | 37 | 60.7 | 125 | 2 | Q9AVZ1 | Q9AVZ1 guillardia |
| 34 | 37 | 60.7 | 151 | 2 | Q8R891 | Q8R891 thermoaer |
| 35 | 37 | 60.7 | 160 | 1 | SCS1_SHEEP | P49928 ovis aries |
| 36 | 37 | 60.7 | 160 | 1 | SCS2_SHEEP | P49929 ovis aries |
| 37 | 37 | 60.7 | 207 | 2 | Q846Q4 | Q846Q4 myxococcus |
| 38 | 37 | 60.7 | 295 | 2 | Q13635 | Q13635 schizosacch |
| 39 | 37 | 60.7 | 301 | 2 | Q86FM8 | Q86FM8 caenorhabd |
| 40 | 37 | 60.7 | 302 | 2 | Q81126 | Q81126 caenorhabd |
| 41 | 37 | 60.7 | 308 | 2 | Q8R2C7 | Q8R2C7 mus musculu |
| 42 | 37 | 60.7 | 352 | 2 | Q9MAB0 | Q9MAB0 arabidopsis |
| 43 | 37 | 60.7 | 354 | 1 | H181_OCEIH | Q86833 oceanobact |
| 44 | 37 | 60.7 | 368 | 1 | Y5F8_BACSU | P94536 bacillus su |
| 45 | 37 | 60.7 | 415 | 2 | Q9SPU4 | Q9SPU4 nicotiana t |

ALIGNMENTS

RESULT 1
TF3B_SCHPO STANDARD; PRT; 500 AA.
AC Q9P6R0; Q9USU4;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Transcription factor IIRB 60 kDa subunit (TFIIRB) (B-related factor)
DE 1 (BRF) (TFIIR-related factor)
GN Name=Brf1; ORFNames=SPBC1387.10c, SPBC30D10.20;
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Felkner T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinovitch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skellon J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Wellens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Borzys K., Langer I., Beck A., Leinach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Medler H., Wambut S., Purrelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Leleaux V., Motter S.,
RA Galibert M., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garcon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez J., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cernutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
RN [2]
RP INTERACTION WITH TBP.
RX MEDLINE=22569152; PubMed=12682361; DOI=10.1093/nar/gk301;
RA Huang Y., McGillicuddy E., Weindel M., Dong S., Marata R.J.;
RT "The fission yeast TFIIR-related factor limits RNA polymerase III to a
RT TBP-dependent pathway of TBP recruitment.";
RL Nucleic Acids Res. 31:2108-2116(2003).
CC -I- FUNCTION: General activator of RNA polymerase III transcription.
CC -I- COFACTOR: Binds 1 zinc ion per subunit (By similarity).

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OM protein - protein search, using SW model

Run on: May 2, 2005, 12:21:40 ; Search time 8.06145 Seconds

(without alignments)
155.160 Million cell updates/sec

Title: US-09-642-744d-15

Perfect score: 61

Sequence: 1 LRRIIRKIHNIK 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 263416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 263416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.79.*
2: PIR1.*
3: PIR2.*
4: PIR3.*
5: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|-----------------------|
| 1 | 39 | 63.9 | 202 | 1 H70318 | conserved hypochet |
| 2 | 39 | 63.9 | 210 | 2 AC1577 | precortin isomeras |
| 3 | 38 | 62.3 | 272 | 2 AB3430 | transposase BME14 |
| 4 | 38 | 62.3 | 284 | 2 A10897 | regucalcin-biphosph |
| 5 | 38 | 62.3 | 623 | 2 S73462 | transport ATP-bind |
| 6 | 38 | 62.3 | 780 | 2 AB1801 | amino-terminal dom |
| 7 | 38 | 62.3 | 1188 | 2 C71231 | hypothetical prote |
| 8 | 37 | 60.7 | 87 | 2 S00180 | spermatid protein |
| 9 | 37 | 60.7 | 125 | 2 A99114 | hypothetical prote |
| 10 | 37 | 60.7 | 152 | 2 S68411 | cathelin-related p |
| 11 | 37 | 60.7 | 160 | 2 S68412 | myeloid antimicrob |
| 12 | 37 | 60.7 | 160 | 2 S68428 | CDS protein F911. |
| 13 | 37 | 60.7 | 352 | 2 H86454 | conserved hypochet |
| 14 | 37 | 60.7 | 368 | 2 C69984 | hypothetical prote |
| 15 | 36 | 59.0 | 41 | 2 S77768 | hypothetical prote |
| 16 | 36 | 59.0 | 337 | 2 S46010 | hypothetical prote |
| 17 | 36 | 59.0 | 357 | 2 S21992 | envelope protein g |
| 18 | 36 | 59.0 | 484 | 2 A70558 | hypothetical prote |
| 19 | 36 | 59.0 | 569 | 2 C83952 | prolyl-L-lysine synth |
| 20 | 36 | 59.0 | 613 | 2 F64056 | probable ATP-depen |
| 21 | 36 | 59.0 | 672 | 2 S46276 | acetate-CoA ligase |
| 22 | 36 | 59.0 | 780 | 2 A11497 | transcription regu |
| 23 | 36 | 59.0 | 8243 | 2 T31307 | type I fatty acid |
| 24 | 35 | 57.4 | 62 | 1 R5BS3F | ribosomal protein |
| 25 | 35 | 57.4 | 155 | 2 AD1883 | hypothetical prote |
| 26 | 35 | 57.4 | 164 | 2 T50602 | ribosomal protein |
| 27 | 35 | 57.4 | 164 | 2 G86230 | hypothetical prote |
| 28 | 35 | 57.4 | 164 | 2 H96610 | probable 60S ribos |
| 29 | 35 | 57.4 | 180 | 2 S39775 | alpha-s2-casein fo |

| | | | | | |
|----|----|------|-----|----------|--------------------|
| 30 | 35 | 57.4 | 212 | 2 A64045 | 2-dehydro-3-deoxy- |
| 31 | 35 | 57.4 | 220 | 2 C53376 | hypothetical prote |
| 32 | 35 | 57.4 | 220 | 2 T22852 | hypothetical prote |
| 33 | 35 | 57.4 | 336 | 2 T31851 | hypothetical prote |
| 34 | 35 | 57.4 | 370 | 2 C70464 | GTP-binding protei |
| 35 | 35 | 57.4 | 381 | 2 F71078 | hypothetical prote |
| 36 | 35 | 57.4 | 437 | 2 C86435 | hypothetical prote |
| 37 | 35 | 57.4 | 483 | 2 S75369 | protein F17F8.15 l |
| 38 | 35 | 57.4 | 519 | 2 B88322 | hypothetical prote |
| 39 | 35 | 57.4 | 519 | 2 T19998 | protein C47D12.8 l |
| 40 | 35 | 57.4 | 522 | 2 T24144 | hypothetical prote |
| 41 | 35 | 57.4 | 529 | 1 X1E8M | hypothetical prote |
| 42 | 35 | 57.4 | 532 | 2 T38326 | site-specific DNA- |
| 43 | 35 | 57.4 | 577 | 2 F64549 | serine threonine p |
| 44 | 35 | 57.4 | 622 | 2 E72754 | proline-cRNA ligas |
| 45 | 35 | 57.4 | 626 | 1 SYNCA | probable phosphoen |
| | | | | | acetate-CoA ligase |

ALIGNMENTS

RESULT 1

H70318 conserved hypothetical protein aq_202 - Aquifex aeolicus

C/Species: Aquifex aeolicus

C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C/Accession: H70318

R/Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; C

V. Nature 392, 353-358, 1998

A/Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.

A/Reference number: A70300; PMID:98196666; PMID:9537320

A/Accession: H70318

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-202 <NOFS>

A/Cross-references: UNIPROT:Q66580; GB:AE000678; NID:G2982921; PIDN:AAC06551.1; PID:G25

A/Experimental source: strain VFS

C/Genetics:

A/Gene: aq_202

C/Superfamily: Methanococcus jannaschii conserved hypothetical protein_M0226

Query Match 63.9%; Score 39; DB 1; Length 202;

Best Local Similarity 45.5%; Pred. No. 20;

Matches 5; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 3 RIRKIHNIK 13

DB 186 RLRKLVHYLK 196

RESULT 2

AC1577 precortin isomerase homolog jln1156 [imported] - Listeria innocua (strain C11p11262)

C/Species: Listeria innocua

C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004

C/Accession: AC1577

R/Glaeser, P.; Frangoul, L.; Buchteler, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker

; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fehrl, H

D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A/Authors: Kref, J.; Kuhn, M.; Kunat, F.; Kurapkat, G.; Madueno, E.; Maitouram, A.; M

ok, C.; Schluter, T.; Simoes, N.; Tietzer, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland

A/Title: Comparative genomics of Listeria species

A/Reference number: AB1077; PMID:21537279; PMID:11679669

A/Accession: AC1577

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-210 <GLA>

A/Cross-references: UNIPROT:Q92CL5; GB:AL592022; PIDN:CA69387.1; PID:gl6413615; GSPDB:

C/Genetics:

A/Gene: jln1156

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OM protein - protein search, using sw model

Run on: May 2, 2005, 13:03:56 ; Search time 35.3687 Seconds

(without alignments)
122.435 Million cell updates/sec

Title: US-09-642-744D-15

Sequence: 61
1 LRRIRKIHIIK 13

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1426032 seqs, 333106140 residues

Total number of hits satisfying chosen parameters: 1426032

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/1/pubppa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubppa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubppa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubppa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubppa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubppa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubppa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubppa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubppa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubppa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubppa/US10A_PUBCOMB.pep:*
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15: /cgn2_6/ptodata/1/pubppa/US10C_PUBCOMB.pep:*
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17: /cgn2_6/ptodata/1/pubppa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubppa/US10_NEW_PUB.pep:*
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20: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|------------------|-------------------|
| 1 | 61 | 100.0 | 14 | US-10-060-102-13 | Sequence 13, Appl |
| 2 | 61 | 100.0 | 14 | US-10-060-102-18 | Sequence 18, Appl |
| 3 | 61 | 100.0 | 14 | US-10-721-839-13 | Sequence 13, Appl |
| 4 | 61 | 100.0 | 14 | US-10-721-839-18 | Sequence 18, Appl |
| 5 | 61 | 100.0 | 16 | US-10-060-102-14 | Sequence 14, Appl |
| 6 | 61 | 100.0 | 16 | US-10-721-839-14 | Sequence 14, Appl |
| 7 | 61 | 100.0 | 18 | US-09-840-009-2 | Sequence 2, Appl |
| 8 | 61 | 100.0 | 18 | US-09-840-009-9 | Sequence 9, Appl |
| 9 | 61 | 100.0 | 18 | US-09-840-009-15 | Sequence 15, Appl |
| 10 | 61 | 100.0 | 18 | US-09-840-009-23 | Sequence 23, Appl |
| 11 | 61 | 100.0 | 18 | US-09-840-009-30 | Sequence 30, Appl |
| 12 | 61 | 100.0 | 18 | US-10-060-102-9 | Sequence 9, Appl |
| 13 | 61 | 100.0 | 18 | US-10-060-102-12 | Sequence 12, Appl |

| | | | | | |
|----|----|-------|----|------------------|-------------------|
| 14 | 61 | 100.0 | 18 | US-10-721-839-9 | Sequence 9, Appl |
| 15 | 61 | 100.0 | 18 | US-10-721-839-12 | Sequence 12, Appl |
| 16 | 61 | 100.0 | 29 | US-10-060-102-8 | Sequence 8, Appl |
| 17 | 61 | 100.0 | 29 | US-10-721-839-8 | Sequence 8, Appl |
| 18 | 59 | 96.7 | 14 | US-10-060-102-19 | Sequence 19, Appl |
| 19 | 59 | 96.7 | 14 | US-10-060-102-20 | Sequence 20, Appl |
| 20 | 59 | 96.7 | 14 | US-10-721-839-19 | Sequence 19, Appl |
| 21 | 59 | 96.7 | 14 | US-10-721-839-20 | Sequence 20, Appl |
| 22 | 59 | 96.7 | 16 | US-10-060-102-15 | Sequence 15, Appl |
| 23 | 59 | 96.7 | 16 | US-10-721-839-15 | Sequence 15, Appl |
| 24 | 59 | 96.7 | 18 | US-10-060-102-10 | Sequence 10, Appl |
| 25 | 59 | 96.7 | 18 | US-10-060-102-11 | Sequence 11, Appl |
| 26 | 59 | 96.7 | 18 | US-10-721-839-10 | Sequence 10, Appl |
| 27 | 59 | 96.7 | 18 | US-10-721-839-11 | Sequence 11, Appl |
| 28 | 56 | 91.8 | 18 | US-09-840-009-4 | Sequence 4, Appl |
| 29 | 56 | 91.8 | 18 | US-09-840-009-11 | Sequence 11, Appl |
| 30 | 56 | 91.8 | 18 | US-09-840-009-15 | Sequence 15, Appl |
| 31 | 56 | 91.8 | 18 | US-09-840-009-18 | Sequence 18, Appl |
| 32 | 56 | 91.8 | 18 | US-09-840-009-22 | Sequence 22, Appl |
| 33 | 56 | 91.8 | 18 | US-09-840-009-25 | Sequence 25, Appl |
| 34 | 56 | 91.8 | 18 | US-09-840-009-26 | Sequence 26, Appl |
| 35 | 56 | 91.8 | 18 | US-09-840-009-6 | Sequence 6, Appl |
| 36 | 56 | 91.8 | 18 | US-10-060-102-25 | Sequence 25, Appl |
| 37 | 56 | 91.8 | 18 | US-10-721-839-25 | Sequence 25, Appl |
| 38 | 55 | 90.2 | 18 | US-09-840-009-5 | Sequence 5, Appl |
| 39 | 55 | 90.2 | 18 | US-09-840-009-12 | Sequence 12, Appl |
| 40 | 55 | 90.2 | 18 | US-09-840-009-19 | Sequence 19, Appl |
| 41 | 55 | 90.2 | 18 | US-09-840-009-26 | Sequence 26, Appl |
| 42 | 54 | 88.5 | 18 | US-09-840-009-7 | Sequence 7, Appl |
| 43 | 54 | 88.5 | 18 | US-09-840-009-13 | Sequence 13, Appl |
| 44 | 54 | 88.5 | 18 | US-09-840-009-14 | Sequence 14, Appl |
| 45 | 54 | 88.5 | 9 | US-10-060-102-13 | Sequence 13, Appl |

ALIGNMENTS

RESULT 1
US-10-060-102-13
; Sequence 13, Application US/10060102
; Publication No. US20030022829A1
; GENERAL INFORMATION:
; APPLICANT: MAURY, WENDY
; APPLICANT: STAPLETON, JACK
; APPLICANT: ROLLER, RICHARD
; APPLICANT: STINSKI, MARK
; APPLICANT: MCCRAY, PAUL B.
; TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMAL
; TITLE OF INVENTION: CATHELICIDINS
; FILE REFERENCE: IOWA:035US
; CURRENT FILING DATE: 2002-02-22
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/309,368
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/265,270
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 13
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-060-102-13

Query Match 100.0%; Score 61; DB 14; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LRRIRKIHIIK 13

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:18:40 ; Search time 12.3464 Seconds
(without alignments)
78.601 Million cell updates/sec

Title: US-09-642-744D-15

Sequence: 1 LRRIRKIRIH1K 13

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
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2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PTCUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|------------------|
| 1 | 61 | 100.0 | 18 | 4 | US-09-840-009-2 |
| 2 | 61 | 100.0 | 18 | 4 | US-09-840-009-9 |
| 3 | 61 | 100.0 | 18 | 4 | US-09-840-009-16 |
| 4 | 61 | 100.0 | 18 | 4 | US-09-840-009-23 |
| 5 | 61 | 100.0 | 18 | 4 | US-09-840-009-30 |
| 6 | 56 | 91.8 | 18 | 4 | US-09-840-009-4 |
| 7 | 56 | 91.8 | 18 | 4 | US-09-840-009-8 |
| 8 | 56 | 91.8 | 18 | 4 | US-09-840-009-11 |
| 9 | 56 | 91.8 | 18 | 4 | US-09-840-009-15 |
| 10 | 56 | 91.8 | 18 | 4 | US-09-840-009-18 |
| 11 | 56 | 91.8 | 18 | 4 | US-09-840-009-22 |
| 12 | 56 | 91.8 | 18 | 4 | US-09-840-009-25 |
| 13 | 56 | 91.8 | 18 | 4 | US-09-840-009-29 |
| 14 | 55 | 90.2 | 18 | 4 | US-09-840-009-5 |
| 15 | 55 | 90.2 | 18 | 4 | US-09-840-009-12 |
| 16 | 55 | 90.2 | 18 | 4 | US-09-840-009-19 |
| 17 | 55 | 90.2 | 18 | 4 | US-09-840-009-26 |
| 18 | 54 | 88.5 | 18 | 4 | US-09-840-009-6 |
| 19 | 54 | 88.5 | 18 | 4 | US-09-840-009-7 |
| 20 | 54 | 88.5 | 18 | 4 | US-09-840-009-13 |
| 21 | 54 | 88.5 | 18 | 4 | US-09-840-009-14 |
| 22 | 54 | 88.5 | 18 | 4 | US-09-840-009-20 |
| 23 | 54 | 88.5 | 18 | 4 | US-09-840-009-21 |
| 24 | 54 | 88.5 | 18 | 4 | US-09-840-009-27 |
| 25 | 54 | 88.5 | 18 | 4 | US-09-840-009-28 |
| 26 | 53 | 86.9 | 18 | 4 | US-09-840-009-3 |
| 27 | 53 | 86.9 | 18 | 4 | US-09-840-009-10 |

| | | | | | | |
|----|----|------|-----|---|---------------------|-------------------|
| 28 | 53 | 86.9 | 18 | 4 | US-09-840-009-17 | Sequence 17, Appl |
| 29 | 53 | 86.9 | 18 | 4 | US-09-840-009-24 | Sequence 24, Appl |
| 30 | 53 | 86.9 | 18 | 4 | US-09-840-009-31 | Sequence 31, Appl |
| 31 | 53 | 86.9 | 18 | 4 | US-09-840-009-34 | Sequence 34, Appl |
| 32 | 53 | 86.9 | 18 | 4 | US-09-840-009-35 | Sequence 35, Appl |
| 33 | 45 | 73.8 | 18 | 4 | US-09-840-009-32 | Sequence 32, Appl |
| 34 | 45 | 73.8 | 18 | 4 | US-09-840-009-33 | Sequence 33, Appl |
| 35 | 45 | 73.8 | 18 | 4 | US-09-840-009-36 | Sequence 36, Appl |
| 36 | 45 | 73.8 | 18 | 4 | US-09-840-009-37 | Sequence 37, Appl |
| 37 | 41 | 67.2 | 18 | 4 | US-09-840-009-1 | Sequence 1, Appl |
| 38 | 39 | 63.9 | 391 | 4 | US-09-134-001C-5234 | Sequence 5234, Ap |
| 39 | 38 | 62.3 | 24 | 4 | US-09-785-059B-5 | Sequence 5, Appl |
| 40 | 38 | 62.3 | 36 | 4 | US-09-785-059B-6 | Sequence 6, Appl |
| 41 | 38 | 62.3 | 42 | 4 | US-09-785-059B-7 | Sequence 7, Appl |
| 42 | 38 | 62.3 | 48 | 4 | US-09-785-059B-8 | Sequence 8, Appl |
| 43 | 37 | 60.7 | 160 | 4 | US-09-917-340-36 | Sequence 36, Appl |
| 44 | 37 | 60.7 | 185 | 4 | US-09-902-540-15903 | Sequence 15903, A |
| 45 | 36 | 59.0 | 337 | 4 | US-09-538-092-38 | Sequence 38, Appl |

ALIGNMENTS

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RESULT 1
US-09-840-009-2
Sequence 2, Application US/09840009
Patent No. 6492328
GENERAL INFORMATION:
APPLICANT: Lehrer, Robert I.
APPLICANT: Waring, Alan J.
TITLE OF INVENTION: NOVISPIRINS: ANTIMICROBIAL PEPTIDES
FILE REFERENCE: 06510-195WO
CURRENT FILING DATE: 2001-04-19
PRIOR APPLICATION NUMBER: US/09/840,009
PRIOR FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 2
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic antimicrobial peptide
US-09-840-009-2

Query Match      100.0%; Score 61; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 LRRIRKIRIH1K 13
Db      3 LRRIRKIRIH1K 15

RESULT 2
US-09-840-009-9
Sequence 9, Application US/09840009
Patent No. 6492328
GENERAL INFORMATION:
APPLICANT: Lehrer, Robert I.
APPLICANT: Waring, Alan J.
TITLE OF INVENTION: NOVISPIRINS: ANTIMICROBIAL PEPTIDES
FILE REFERENCE: 06510-195WO
CURRENT FILING DATE: 2001-04-19
PRIOR APPLICATION NUMBER: US/09/840,009
PRIOR FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 9
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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:17:55 ; Search time 45.5726 Seconds

(without alignments)
110.327 Million cell updates/sec

Title: US-09-642-744D-15
Perfect score: 61
Sequence: 1 LRRIRKIRIK 13

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: A_Geneseq_16Dec04:*
2: geneseqp1980s:*
3: geneseqp1990s:*
4: geneseqp2000s:*
5: geneseqp2001s:*
6: geneseqp2002s:*
7: geneseqp2003as:*
8: geneseqp2003bs:*
9: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|-------------|--------------------|
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| 2 | 61 | 100.0 | 14 | 4 AAB70658 | Aab70658 Ovine SMA |
| 3 | 61 | 100.0 | 14 | 4 AAB70659 | Aab70659 Ovine SMA |
| 4 | 61 | 100.0 | 14 | 5 AABP53280 | Abp53280 Synthetic |
| 5 | 61 | 100.0 | 14 | 5 AABP53285 | Abp53285 Synthetic |
| 6 | 61 | 100.0 | 16 | 4 AAB70656 | Aab70656 Ovine SMA |
| 7 | 61 | 100.0 | 16 | 5 AABP53281 | Abp53281 Synthetic |
| 8 | 61 | 100.0 | 18 | 4 AAB70655 | Aab70655 Ovine SMA |
| 9 | 61 | 100.0 | 18 | 4 AAB70648 | Aab70648 Ovine SMA |
| 10 | 61 | 100.0 | 18 | 5 AAE20882 | Aae20882 D11-nov1 |
| 11 | 61 | 100.0 | 18 | 5 AAE20875 | Aae20875 D110-nov1 |
| 12 | 61 | 100.0 | 18 | 5 AAE20854 | Aae20854 Ovisplrin |
| 13 | 61 | 100.0 | 18 | 5 AAE20861 | Aae20861 D16-nov1s |
| 14 | 61 | 100.0 | 18 | 5 AAE20868 | Aae20868 D17-nov1s |
| 15 | 61 | 100.0 | 18 | 5 AABP53276 | Abp53276 Synthetic |
| 16 | 61 | 100.0 | 18 | 5 AABP53279 | Abp53279 Synthetic |
| 17 | 61 | 100.0 | 29 | 4 AAB70675 | Aab70675 Ovine SMA |
| 18 | 61 | 100.0 | 29 | 5 AABP53275 | Abp53275 Synthetic |
| 19 | 59 | 96.7 | 14 | 4 AAB70661 | Aab70661 Ovine SMA |
| 20 | 59 | 96.7 | 14 | 4 AAB70660 | Aab70660 Ovine SMA |
| 21 | 59 | 96.7 | 14 | 5 AABP53286 | Abp53286 Synthetic |
| 22 | 59 | 96.7 | 14 | 5 AABP53287 | Abp53287 Synthetic |
| 23 | 59 | 96.7 | 16 | 4 AAB70657 | Aab70657 Ovine SMA |
| 24 | 59 | 96.7 | 16 | 5 AABP53282 | Abp53282 Synthetic |
| 25 | 59 | 96.7 | 18 | 4 AAB70654 | Aab70654 Ovine SMA |

| | | | | | |
|----|----|------|----|-------------|--------------------|
| 26 | 59 | 96.7 | 18 | 5 AABP53278 | Abp53278 Synthetic |
| 27 | 59 | 96.7 | 18 | 5 AABP53277 | Abp53277 Synthetic |
| 28 | 59 | 96.7 | 20 | 4 AAB70653 | Aab70653 Ovine SMA |
| 29 | 57 | 93.4 | 12 | 4 AAB70664 | Aab70664 Ovine SMA |
| 30 | 57 | 93.4 | 13 | 4 AAB70663 | Aab70663 Ovine SMA |
| 31 | 56 | 91.8 | 18 | 5 AAE20870 | Aae20870 D11-nov1s |
| 32 | 56 | 91.8 | 18 | 5 AAE20860 | Aae20860 D16-nov1s |
| 33 | 56 | 91.8 | 18 | 5 AAE20881 | Aae20881 D11-nov1 |
| 34 | 56 | 91.8 | 18 | 5 AAE20867 | Aae20867 D17-nov1s |
| 35 | 56 | 91.8 | 18 | 5 AAE20874 | Aae20874 D110-nov1 |
| 36 | 56 | 91.8 | 18 | 5 AAE20863 | Aae20863 T7-nov1s |
| 37 | 56 | 91.8 | 18 | 5 AAE20877 | Aae20877 T11-nov1s |
| 38 | 56 | 91.8 | 18 | 5 AAE20856 | Aae20856 T6-nov1s |
| 39 | 56 | 91.8 | 18 | 5 AABP53292 | Abp53292 Synthetic |
| 40 | 55 | 90.2 | 18 | 5 AAE20864 | Aae20864 S7-nov1s |
| 41 | 55 | 90.2 | 18 | 5 AAE20871 | Aae20871 S10-nov1s |
| 42 | 55 | 90.2 | 18 | 5 AAE20878 | Aae20878 S11-nov1s |
| 43 | 55 | 90.2 | 18 | 5 AAE20857 | Aae20857 S6-nov1s |
| 44 | 54 | 88.5 | 18 | 5 AAE20872 | Aae20872 E10-nov1s |
| 45 | 54 | 88.5 | 18 | 5 AAE20873 | Aae20873 D10-nov1s |

ALIGNMENTS

| | | |
|----------|---|------------------------------------|
| RESULT 1 | AAB70662 | AAB70662 standard; peptide; 13 AA. |
| ID | AAB70662 | |
| XX | 15-MAY-2001 (first entry) | |
| XX | Ovine SNAP 29 cathelicidin derived antimicrobial peptide SEQ ID NO:15. | |
| DE | XX | |
| XX | Ovine: SMA29, lupine: RCAP 18, cathelicidin, antimicrobial; | |
| KW | bactericidal; antibiotic; antiviral; microbial growth inhibitor; | |
| KW | proliferation inhibitor; gene therapy; Pseudomonas aeruginosa; | |
| KW | Burkholderia cepacia; Alcaligenes; Xanthomonas. | |
| XX | XX | |
| OS | Ovis aries. | |
| PN | WO200112668-A1. | |
| XX | 22-FEB-2001. | |
| PD | 18-AUG-2000; 2000WO-US022781. | |
| XX | 18-AUG-1999; 99US-0149886P. | |
| PR | (IOWA) UNIV IOWA RES FOUND. | |
| PA | (REGC) UNIV CALIFORNIA. | |
| PA | Tack BE, Mccravy P, Welsh M, Travis SM, Lehrer R; | |
| PI | WPI; 2001-234911/24. | |
| DR | New antimicrobial peptides useful as antibiotics for inhibiting growth | |
| XX | and proliferation of microbes, and for treating microbial infections. | |
| PT | Claim 1, Page 103; 137pp; English. | |
| PS | AAB70648 to AAB70675 represent antimicrobial peptides (I), of which | |
| CC | AAB70648 to AAB70664, AAB70674 and AAB70675 are derived from the ovine | |
| CC | SNAP 29 cathelicidin family peptide, and AAB70665 to AAB70673 are derived | |
| CC | from the lupine RCAP 18 cathelicidin family peptide. (I) have antibiotic, | |
| CC | antimicrobial and antiviral activities, and can be used as microbial | |
| CC | growth and proliferation inhibitors and in gene therapy. (I) are useful | |
| CC | for inhibiting microbial growth in an environment capable of sustaining | |
| CC | such growth, for inhibiting microbial growth or strain in a host, and | |
| CC | inhibiting the growth of drug-resistant microbial strains such as | |
| CC | Pseudomonas aeruginosa, Burkholderia cepacia, Alcaligenes and Xanthomonas | |
| XX | | |

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:17:06 ; Search time 43.6816 Seconds

(without alignments)
164.122 Million cell updates/sec

Title: US-09-642-744d-14

Perfect score: 66

Sequence: 1 IRRIRKIHITKK 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues 1612378

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 1 | 65.2 | 638 | 2 QBD796 | QBD796 vibrio vuln |
| 2 | 65.2 | 660 | 2 Q7MEAO | Q7MEAO vibrio vuln |
| 3 | 63.6 | 125 | 2 Q9AVZ1 | Q9AVZ1 guillardi |
| 4 | 63.6 | 308 | 2 QBR2C7 | QBR2C7 mus musculu |
| 5 | 63.6 | 414 | 2 Q947U2 | Q947U2 oryza sativ |
| 6 | 63.6 | 414 | 2 Q7XBY8 | Q7XBY8 oryza sativ |
| 7 | 63.6 | 500 | 1 TR3B_SCHPO | Q9P6T0 schizosacch |
| 8 | 63.6 | 867 | 2 Q283J1 | Q283J1 archaeoglob |
| 9 | 62.1 | 337 | 1 YB21_YEAST | P38278 baccharomyc |
| 10 | 62.1 | 428 | 2 Q8TXS5 | Q8TXS5 methanopyru |
| 11 | 62.1 | 613 | 1 DEAD_HA2IN | P45868 haemophilus |
| 12 | 62.1 | 670 | 1 REP_BUCBP | Q89821 buchiera ap |
| 13 | 62.1 | 1580 | 2 Q7RMP4 | Q7RMP4 plasmodium |
| 14 | 62.1 | 2084 | 2 Q8ILJ6 | Q8ILJ6 plasmodium |
| 15 | 60.6 | 151 | 2 Q8R891 | Q8R891 thermoanaer |
| 16 | 60.6 | 160 | 1 SC51_SHEEP | P49928 ovis aries |
| 17 | 60.6 | 240 | 1 SC52_SHEEP | P49928 ovis aries |
| 18 | 60.6 | 240 | 1 Q7NSJ3 | Q7NSJ3 photorhabdu |
| 19 | 60.6 | 256 | 2 Q83CP2 | Q83CP2 coxiella bu |
| 20 | 60.6 | 328 | 2 Q7Z1V1 | Q7Z1V1 leptospira |
| 21 | 60.6 | 328 | 2 Q8F1B9 | Q8F1B9 leptospira |
| 22 | 60.6 | 370 | 2 Q7N787 | Q7N787 aquifex aeo |
| 23 | 60.6 | 452 | 2 Q7N787 | Q7N787 aquifex aeo |
| 24 | 60.6 | 475 | 2 Q7SGI8 | Q7SGI8 oryza sativ |
| 25 | 60.6 | 671 | 2 Q8Q0U6 | Q8Q0U6 methanosaic |
| 26 | 60.6 | 822 | 2 Q8ZMW0 | Q8ZMW0 pyrobaculum |
| 27 | 59.1 | 41 | 2 Q48971 | Q48971 mycoplasma |
| 28 | 59.1 | 202 | 1 HAM1_AQUAE | Q66580 aquifex aeo |
| 29 | 59.1 | 210 | 2 Q92CL5 | Q92CL5 listeria in |
| 30 | 59.1 | 217 | 2 Q977R2 | Q977R2 uncultured |
| 31 | 59.1 | 250 | 2 Q7W5F0 | Q7W5F0 bordetella |

| | | | | | |
|----|----|------|-----|--------------|---------------------|
| 32 | 39 | 59.1 | 250 | 2 Q7WCY5 | Q7WCY5 bordetella |
| 33 | 39 | 59.1 | 258 | 2 Q8MY71 | Q8MY71 brachionus |
| 34 | 39 | 59.1 | 295 | 2 Q13635 | Q13635 schizosacch |
| 35 | 39 | 59.1 | 354 | 1 H181_OCEIH | Q88833 oceanobacill |
| 36 | 39 | 59.1 | 407 | 2 Q9UTH1 | Q9UTH1 schizosacch |
| 37 | 39 | 59.1 | 415 | 2 Q8SPU4 | Q8SPU4 nicotiana t |
| 38 | 39 | 59.1 | 460 | 2 Q8VLO3 | Q8VLO3 dirosophila |
| 39 | 39 | 59.1 | 461 | 2 Q8IBM2 | Q8IBM2 plasmodium |
| 40 | 39 | 59.1 | 483 | 2 Q9KRA1 | Q9KRA1 vibrio chol |
| 41 | 39 | 59.1 | 549 | 2 Q8IPR2 | Q8IPR2 dirosophila |
| 42 | 39 | 59.1 | 598 | 2 Q7VTH0 | Q7VTH0 bordetella |
| 43 | 39 | 59.1 | 647 | 2 Q6Z647 | Q6Z647 oryza sativ |
| 44 | 39 | 59.1 | 834 | 2 Q6FW11 | Q6FW11 candida gla |
| 45 | 39 | 59.1 | 866 | 2 Q8JDU9 | Q8JDU9 human immun |

ALIGNMENTS

RESULT 1

QBD796 PRELIMINARY; PRT; 638 AA.

AC QBD796; 01-MAR-2003 (TRMBLrel. 23, Created)

DT 01-MAR-2003 (TRMBLrel. 23, Last sequence update)

DE 01-MAR-2004 (TRMBLrel. 26, Last annotation update)

GN Predicted signal transduction protein.

OC OrderedLocustNames=VV20264;

OS Vibrio vulnificus.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;

OC Vibrionaceae; Vibrio.

OX NCBI_TaxID=672;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CMCP6;

RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,

Choy H.E.;

RT "Complete genome sequence of Vibrio vulnificus CMCP6.";

RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AE016808; AA007230.1; --

DR InterPro; IPR001633; EAL.

DR InterPro; IPR003018; GAF.

DR Pfam; PF00563; EAL; 1.

DR Pfam; PF01590; GAF; 1.

DR Pfam; PF00990; GDEF; 1.

DR SMART; SM00052; DUF2; 1.

DR SMART; SM00065; GAF; 1.

DR TIGRFAMs; TIGR00254; GDEF; 1.

DR PROSITE; PS50883; EAL; 1.

DR PROSITE; PS50887; GDEF; 1.

KW Complete proteome.

SO SEQUENCE 638 AA; 72187 MW; 7D13E28DF3A3F099 CRC64;

Query Match Best Local Similarity 65.2%; Score 43; DB 2; Length 638;

Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 RRIIRKIHITKK 14

Db 566 KEIRIRSIHVAKK 578

QY 2 RRIIRKIHITKK 14

Db 566 KEIRIRSIHVAKK 578

QY 2 RRIIRKIHITKK 14

Db 566 KEIRIRSIHVAKK 578

QY 2 RRIIRKIHITKK 14

Db 566 KEIRIRSIHVAKK 578

QY 2 RRIIRKIHITKK 14

Db 566 KEIRIRSIHVAKK 578

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:21:40 ; Search time 8.68156 seconds

(without alignments)
155.160 Million cell updates/sec

Title: US-09-642-744D-14

Perfect score: 66

Sequence: 1 IRRIRKIHIIKK 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: PIR 79:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 42 | 63.6 | 125 | 2 A99114 | hypothetical prote |
| 2 | 42 | 63.6 | 867 | 2 G69485 | DNA-directed RNA p |
| 3 | 41 | 62.1 | 337 | 2 S46010 | hypothetical prote |
| 4 | 41 | 62.1 | 613 | 2 P64056 | probable ATP-depen |
| 5 | 40 | 60.6 | 152 | 2 S68411 | cathelin-related p |
| 6 | 40 | 60.6 | 160 | 2 S68412 | myeloid antimicrob |
| 7 | 40 | 60.6 | 160 | 2 S68228 | GTP-binding protei |
| 8 | 39 | 59.1 | 41 | 2 S77768 | hypothetical prote |
| 9 | 39 | 59.1 | 202 | 1 H70318 | conserved hypotet |
| 10 | 39 | 59.1 | 210 | 2 AC1577 | precortin isomeras |
| 11 | 39 | 59.1 | 407 | 2 T37888 | hypothetical prote |
| 12 | 39 | 59.1 | 483 | 2 B82160 | hypothetical prote |
| 13 | 39 | 59.1 | 87 | 2 S00180 | spermatid protein |
| 14 | 38 | 57.6 | 234 | 2 D97108 | DNA-dependent RNA |
| 15 | 38 | 57.6 | 234 | 2 D97108 | sigk protein - Cio |
| 16 | 38 | 57.6 | 234 | 2 D97108 | transposase BME114 |
| 17 | 38 | 57.6 | 234 | 2 D97108 | transport ATP-bind |
| 18 | 38 | 57.6 | 234 | 2 D97108 | helicase (BC 3.6.1 |
| 19 | 38 | 57.6 | 234 | 2 D97108 | 2-dehydro-3-deoxy- |
| 20 | 38 | 57.6 | 234 | 2 D97108 | tagatose-bisphosph |
| 21 | 37 | 56.1 | 62 | 1 R5B53F | hypothetical prote |
| 22 | 37 | 56.1 | 212 | 2 A64045 | ribosomal protein |
| 23 | 37 | 56.1 | 284 | 2 A10897 | 2-dehydro-3-deoxy- |
| 24 | 37 | 56.1 | 303 | 2 P71212 | hypothetical prote |
| 25 | 37 | 56.1 | 324 | 2 B72201 | endoglucanase - Th |
| 26 | 37 | 56.1 | 364 | 2 C70322 | 3-isopropylmalate |
| 27 | 37 | 56.1 | 368 | 2 C69984 | conserved hypotet |
| 28 | 37 | 56.1 | 483 | 2 S75369 | DNA primase chain |
| 29 | 37 | 56.1 | 569 | 2 C83952 | hypothetical prote |

| | | | | | |
|----|----|------|------|----------|--------------------|
| 30 | 37 | 56.1 | 813 | 2 T20527 | hypothetical prote |
| 31 | 37 | 56.1 | 856 | 1 VCLJ3W | env polyprotein pr |
| 32 | 36 | 54.5 | 67 | 2 B72248 | ribosomal protein |
| 33 | 36 | 54.5 | 102 | 2 AD1420 | PTS cellobiose-spe |
| 34 | 36 | 54.5 | 102 | 2 AE1795 | PTS cellobiose-spe |
| 35 | 36 | 54.5 | 117 | 2 T12722 | hypothetical prote |
| 36 | 36 | 54.5 | 299 | 2 G72307 | hypothetical prote |
| 37 | 36 | 54.5 | 310 | 2 A33489 | hypothetical prote |
| 38 | 36 | 54.5 | 370 | 2 A05034 | hypothetical prote |
| 39 | 36 | 54.5 | 447 | 2 F81678 | hypothetical prote |
| 40 | 36 | 54.5 | 499 | 2 G84972 | GTP-binding protei |
| 41 | 36 | 54.5 | 627 | 2 C82418 | leucyl aminopeptid |
| 42 | 36 | 54.5 | 760 | 2 T24521 | GGDEF family prote |
| 43 | 36 | 54.5 | 780 | 2 AB1801 | hypothetical prote |
| 44 | 36 | 54.5 | 849 | 2 A96592 | amino-terminal dom |
| 45 | 36 | 54.5 | 1188 | 2 C71231 | hypothetical prote |

ALIGNMENTS

RESULT 1

A99114 hypothetical protein orf125 [imported] - Guillardia theta nucleomorph

C:Species: nucleomorph Guillardia theta

A:Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont

C:Date: 10-May-2001 #sequence_revision 10-May-2001 #ext_change 09-Jul-2004

C:Accession: A99114

R:Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Re

Nature 410, 1091-1096, 2001

A:Title: The highly reduced genome of an enslaved algal nucleus.

A:Reference number: A99082; MUID:11323671; PMID:11323671

A:Accession: A99114

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-125 <DOU>

A:Cross-references: UNIPROT:Q9AVZ1; GB:AJ010592; NID:g12580762; PIDN:CAC27080.1; GSPDB:

C:Gene: orf125

A:Gene position: 2

A:Genome: nucleomorph

C:Keywords: nucleomorph

Query Match

Best Local Similarity 63.6%; Score 42; DB 2; Length 125;

Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 5 IRRIRKIHIIKK 14

DB 9 IRRIRKIHIIKK 18

RESULT 2

G69485 DNA-directed RNA polymerase, subunit A' (rpoA1) homolog - Archaeoglobus fulgidus

C:Species: Archaeoglobus fulgidus

C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #ext_change 09-Jul-2004

C:Accession: G69485

R:Kleck, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodso

., F.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirsner, S.F

Nature 390, 364-370, 1997

A:Authors: Utechtback, T.; Cotton, M.D.; Spriggs, T.; Attlich, P.; Kaine, B.P.; Sykes, S

Smith, H.O.; Weese, C.R.; Venter, J.C.

A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae

A:Reference number: A69250; MUID:98049343; PMID:9389475

A:Accession: G69485

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-867 <KLE>

A:Cross-references: UNIPROT:Q23191; GB:AE000972; GB:AE000782; NID:g2689295; PIDN:AA893

C:Superfamily: Halobacterium DNA-directed RNA polymerase chain A

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 2, 2005, 13:03:56 ; Search time 38.0894 Seconds,
(without alignments)
122.435 Million cell updates/sec

Title: US-09-642-744D-14
Perfect score: 66
Sequence: 1 IRRIRKIHITIK 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1426032 seqs, 333106140 residues

Total number of hits satisfying chosen parameters: 1426032

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 2 | 66 | 100.0 | 14 | 14 | US-10-060-102-20 |
| 3 | 66 | 100.0 | 14 | 14 | US-10-721-839-19 |
| 4 | 66 | 100.0 | 14 | 14 | US-10-721-839-20 |
| 5 | 66 | 100.0 | 16 | 14 | US-10-060-102-15 |
| 6 | 66 | 100.0 | 16 | 15 | US-10-721-839-15 |
| 7 | 66 | 100.0 | 18 | 14 | US-10-060-102-10 |
| 8 | 66 | 100.0 | 18 | 14 | US-10-060-102-11 |
| 9 | 66 | 100.0 | 18 | 15 | US-10-721-839-10 |
| 10 | 66 | 100.0 | 18 | 15 | US-10-721-839-11 |
| 11 | 64 | 97.0 | 14 | 14 | US-10-060-102-13 |
| 12 | 64 | 97.0 | 14 | 14 | US-10-060-102-18 |
| 13 | 64 | 97.0 | 14 | 15 | US-10-721-839-13 |

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|----|----|------|----|----|------------------|-------------------|
| 14 | 64 | 97.0 | 14 | 15 | US-10-721-839-18 | Sequence 18, Appl |
| 15 | 64 | 97.0 | 16 | 14 | US-10-060-102-14 | Sequence 14, Appl |
| 16 | 64 | 97.0 | 16 | 15 | US-10-721-839-14 | Sequence 14, Appl |
| 17 | 64 | 97.0 | 18 | 9 | US-09-840-009-2 | Sequence 2, Appl |
| 18 | 64 | 97.0 | 18 | 9 | US-09-840-009-9 | Sequence 9, Appl |
| 19 | 64 | 97.0 | 18 | 9 | US-09-840-009-16 | Sequence 16, Appl |
| 20 | 64 | 97.0 | 18 | 9 | US-09-840-009-23 | Sequence 23, Appl |
| 21 | 64 | 97.0 | 18 | 9 | US-09-840-009-30 | Sequence 30, Appl |
| 22 | 64 | 97.0 | 18 | 14 | US-10-060-102-9 | Sequence 9, Appl |
| 23 | 64 | 97.0 | 18 | 14 | US-10-060-102-12 | Sequence 12, Appl |
| 24 | 64 | 97.0 | 18 | 15 | US-10-721-839-9 | Sequence 9, Appl |
| 25 | 64 | 97.0 | 18 | 15 | US-10-721-839-12 | Sequence 12, Appl |
| 26 | 64 | 97.0 | 29 | 14 | US-10-060-102-8 | Sequence 8, Appl |
| 27 | 64 | 97.0 | 29 | 15 | US-10-721-839-8 | Sequence 8, Appl |
| 28 | 59 | 89.4 | 18 | 9 | US-09-840-009-4 | Sequence 4, Appl |
| 29 | 59 | 89.4 | 18 | 9 | US-09-840-009-8 | Sequence 8, Appl |
| 30 | 59 | 89.4 | 18 | 9 | US-09-840-009-11 | Sequence 11, Appl |
| 31 | 59 | 89.4 | 18 | 9 | US-09-840-009-15 | Sequence 15, Appl |
| 32 | 59 | 89.4 | 18 | 9 | US-09-840-009-18 | Sequence 18, Appl |
| 33 | 59 | 89.4 | 18 | 9 | US-09-840-009-22 | Sequence 22, Appl |
| 34 | 59 | 89.4 | 18 | 9 | US-09-840-009-25 | Sequence 25, Appl |
| 35 | 59 | 89.4 | 18 | 9 | US-09-840-009-29 | Sequence 29, Appl |
| 36 | 59 | 89.4 | 18 | 14 | US-10-060-102-25 | Sequence 25, Appl |
| 37 | 59 | 89.4 | 18 | 15 | US-10-721-839-25 | Sequence 25, Appl |
| 38 | 58 | 87.9 | 18 | 9 | US-09-840-009-5 | Sequence 5, Appl |
| 39 | 58 | 87.9 | 18 | 9 | US-09-840-009-12 | Sequence 12, Appl |
| 40 | 58 | 87.9 | 18 | 9 | US-09-840-009-19 | Sequence 19, Appl |
| 41 | 58 | 87.9 | 18 | 9 | US-09-840-009-26 | Sequence 26, Appl |
| 42 | 57 | 86.4 | 18 | 9 | US-09-840-009-6 | Sequence 6, Appl |
| 43 | 57 | 86.4 | 18 | 9 | US-09-840-009-7 | Sequence 7, Appl |
| 44 | 57 | 86.4 | 18 | 9 | US-09-840-009-13 | Sequence 13, Appl |
| 45 | 57 | 86.4 | 18 | 9 | US-09-840-009-14 | Sequence 14, Appl |

ALIGNMENTS

RESULT 1
US-10-060-102-19
; Sequence 19, Application US/10060102
; Publication No. US20030022829A1
; GENERAL INFORMATION:
; APPLICANT: MAURY, WENDY
; APPLICANT: STABLETON, JACK
; APPLICANT: ROLLER, RICHARD
; APPLICANT: STINSKI, MARK
; APPLICANT: MCCRAY, PAUL B.
; TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMA
; FILE REFERENCE: IOWA:035US
; CURRENT APPLICATION NUMBER: US/10/060,102
; PRIOR FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 60/309,368
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/265,270
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; US-10-060-102-19

Query Match 100.0%; Score 66; DB 14; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00056;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 IRRIRKIHITIK 14

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 2, 2005, 12:18:40 ; Search time 13.2961 Seconds

(without alignments)
78.601 Million cell updates/sec

Title: US-09-642-744D-14

Perfect score: 66

Sequence: 1 IRRIRKTIHIKK 14

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: Issued Patents AA:
2: /cgn2_6/prodata/1/1aa/5A COMB pep.*
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4: /cgn2_6/prodata/1/1aa/6A COMB pep.*
5: /cgn2_6/prodata/1/1aa/6B COMB pep.*
6: /cgn2_6/prodata/1/1aa/PCITUS COMB pep.*
7: /cgn2_6/prodata/1/1aa/backf1eal pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 2 | 64 | 97.0 | 18 | 4 | US-09-840-009-9 |
| 3 | 64 | 97.0 | 18 | 4 | US-09-840-009-16 |
| 4 | 64 | 97.0 | 18 | 4 | US-09-840-009-23 |
| 5 | 64 | 97.0 | 18 | 4 | US-09-840-009-30 |
| 6 | 59 | 89.4 | 18 | 4 | US-09-840-009-4 |
| 7 | 59 | 89.4 | 18 | 4 | US-09-840-009-8 |
| 8 | 59 | 89.4 | 18 | 4 | US-09-840-009-11 |
| 9 | 59 | 89.4 | 18 | 4 | US-09-840-009-15 |
| 10 | 59 | 89.4 | 18 | 4 | US-09-840-009-18 |
| 11 | 59 | 89.4 | 18 | 4 | US-09-840-009-22 |
| 12 | 59 | 89.4 | 18 | 4 | US-09-840-009-25 |
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| 14 | 58 | 87.9 | 18 | 4 | US-09-840-009-5 |
| 15 | 58 | 87.9 | 18 | 4 | US-09-840-009-12 |
| 16 | 58 | 87.9 | 18 | 4 | US-09-840-009-19 |
| 17 | 58 | 87.9 | 18 | 4 | US-09-840-009-26 |
| 18 | 57 | 86.4 | 18 | 4 | US-09-840-009-6 |
| 19 | 57 | 86.4 | 18 | 4 | US-09-840-009-7 |
| 20 | 57 | 86.4 | 18 | 4 | US-09-840-009-13 |
| 21 | 57 | 86.4 | 18 | 4 | US-09-840-009-14 |
| 22 | 57 | 86.4 | 18 | 4 | US-09-840-009-20 |
| 23 | 57 | 86.4 | 18 | 4 | US-09-840-009-21 |
| 24 | 57 | 86.4 | 18 | 4 | US-09-840-009-27 |
| 25 | 57 | 86.4 | 18 | 4 | US-09-840-009-28 |
| 26 | 56 | 84.8 | 18 | 4 | US-09-840-009-3 |
| 27 | 56 | 84.8 | 18 | 4 | US-09-840-009-10 |

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| 28 | 56 | 84.8 | 18 | 4 | US-09-840-009-17 | Sequence 17, Appl |
| 29 | 56 | 84.8 | 18 | 4 | US-09-840-009-24 | Sequence 24, Appl |
| 30 | 56 | 84.8 | 18 | 4 | US-09-840-009-31 | Sequence 31, Appl |
| 31 | 56 | 84.8 | 18 | 4 | US-09-840-009-34 | Sequence 34, Appl |
| 32 | 56 | 84.8 | 18 | 4 | US-09-840-009-35 | Sequence 35, Appl |
| 33 | 48 | 72.7 | 18 | 4 | US-09-840-009-32 | Sequence 32, Appl |
| 34 | 48 | 72.7 | 18 | 4 | US-09-840-009-33 | Sequence 33, Appl |
| 35 | 48 | 72.7 | 18 | 4 | US-09-840-009-36 | Sequence 36, Appl |
| 36 | 48 | 72.7 | 18 | 4 | US-09-840-009-37 | Sequence 37, Appl |
| 37 | 44 | 66.7 | 18 | 4 | US-09-840-009-1 | Sequence 1, Appl |
| 38 | 42 | 63.6 | 24 | 4 | US-09-785-0598-5 | Sequence 5, Appl |
| 39 | 42 | 63.6 | 36 | 4 | US-09-785-0598-6 | Sequence 6, Appl |
| 40 | 42 | 63.6 | 42 | 4 | US-09-785-0598-7 | Sequence 7, Appl |
| 41 | 42 | 63.6 | 48 | 4 | US-09-785-0598-8 | Sequence 8, Appl |
| 42 | 41 | 62.1 | 337 | 4 | US-09-538-092-38 | Sequence 38, Appl |
| 43 | 41 | 62.1 | 391 | 3 | US-09-134-001C-5234 | Sequence 5234, Ap |
| 44 | 40 | 60.6 | 160 | 4 | US-09-917-340-36 | Sequence 36, Appl |
| 45 | 40 | 60.6 | 169 | 4 | US-09-270-767-35406 | Sequence 35406, A |

ALIGNMENTS

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RESULT 1
US-09-840-009-2
; Sequence 2, Application US/09840009
; Patent No. 6492328
; GENERAL INFORMATION:
; APPLICANT: Lebrer, Robert I.
; APPLICANT: Waring, Alan J.
; TITLE OF INVENTION: NOVISPIRINS: ANTIMICROBIAL PEPTIDES
; FILE REFERENCE: 06510-195WO
; CURRENT APPLICATION NUMBER: US/09/840,009
; PRIOR FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 09/606,858
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic antimicrobial peptide
US-09-840-009-2
Query Match          97.0%; Score 64; DB 4; Length 18;
Best Local Similarity 92.9%; Pred. No. 0.00098;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY      1 IRRIRKTIHIKK 14
DB      3 LRRIRKTIHIKK 16
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US-09-840-009-9
; Sequence 9, Application US/09840009
; Patent No. 6492328
; GENERAL INFORMATION:
; APPLICANT: Lebrer, Robert I.
; APPLICANT: Waring, Alan J.
; APPLICANT: Tack, Brian F.
; TITLE OF INVENTION: NOVISPIRINS: ANTIMICROBIAL PEPTIDES
; FILE REFERENCE: 06510-195WO
; CURRENT APPLICATION NUMBER: US/09/840,009
; PRIOR FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 09/606,858
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 9
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: May 2, 2005, 12:17:55 ; Search time 49.0782 Seconds
(without alignments)
110.327 Million cell updates/sec

Title: US-09-642-744d-14
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Sequence: 1 IRRIRKIHIIKK 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: geneseqp20008.*
4: geneseqp20018.*
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6: geneseqp20038.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 2 | 66 | 100.0 | 14 | 4 | AAB70660 Aab70660 Ovine SMA |
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| 4 | 66 | 100.0 | 14 | 5 | ABP53287 Abp53287 Synthetic |
| 5 | 66 | 100.0 | 16 | 4 | AAB70657 Aab70657 Ovine SMA |
| 6 | 66 | 100.0 | 16 | 5 | ABP53282 Abp53282 Synthetic |
| 7 | 66 | 100.0 | 18 | 4 | AAB70654 Aab70654 Ovine SMA |
| 8 | 66 | 100.0 | 18 | 5 | ABP53278 Abp53278 Synthetic |
| 9 | 66 | 100.0 | 18 | 5 | ABP53277 Abp53277 Synthetic |
| 10 | 66 | 100.0 | 20 | 4 | AAB70653 Aab70653 Ovine SMA |
| 11 | 66 | 97.0 | 14 | 4 | AAB70658 Aab70658 Ovine SMA |
| 12 | 64 | 97.0 | 14 | 4 | AAB70659 Aab70659 Ovine SMA |
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| 15 | 64 | 97.0 | 16 | 4 | AAB70656 Aab70656 Ovine SMA |
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| 19 | 64 | 97.0 | 18 | 5 | AAE20882 Aae20882 DI11-novi |
| 20 | 64 | 97.0 | 18 | 5 | AAE20885 Aae20885 DI10-novi |
| 21 | 64 | 97.0 | 18 | 5 | AAE20875 Aae20875 DI6-novis |
| 22 | 64 | 97.0 | 18 | 5 | AAE20861 Aae20861 DI7-novis |
| 23 | 64 | 97.0 | 18 | 5 | AAE20868 Aae20868 DI7-novis |
| 24 | 64 | 97.0 | 18 | 5 | ABP53276 Abp53276 Synthetic |
| 25 | 64 | 97.0 | 18 | 5 | ABP53279 Abp53279 Synthetic |

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| 25 | 64 | 97.0 | 29 | 4 | AAB70675 Aab70675 Ovine SMA |
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| 28 | 62 | 93.9 | 13 | 4 | AAB70663 Aab70663 Ovine SMA |
| 29 | 59 | 89.4 | 13 | 4 | AAB70662 Aab70662 Ovine SMA |
| 30 | 59 | 89.4 | 18 | 5 | AAE20870 Aae20870 T10-novis |
| 31 | 59 | 89.4 | 18 | 5 | AAE20860 Aae20860 DA6-novis |
| 32 | 59 | 89.4 | 18 | 5 | AAE20881 Aae20881 DA11-novis |
| 33 | 59 | 89.4 | 18 | 5 | AAE20867 Aae20867 T6-novisp |
| 34 | 59 | 89.4 | 18 | 5 | AAE20874 Aae20874 DA10-novi |
| 35 | 59 | 89.4 | 18 | 5 | AAE20863 Aae20863 T7-novisp |
| 36 | 59 | 89.4 | 18 | 5 | AAE20856 Aae20856 T6-novisp |
| 37 | 59 | 89.4 | 18 | 5 | ABP53292 Abp53292 Synthetic |
| 38 | 59 | 89.4 | 18 | 5 | AAE20871 Aae20871 S10-novis |
| 39 | 58 | 87.9 | 18 | 5 | AAE20864 Aae20864 S11-novis |
| 40 | 58 | 87.9 | 18 | 5 | AAE20878 Aae20878 S6-novisp |
| 41 | 58 | 87.9 | 18 | 5 | AAB70664 Aab70664 Ovine SMA |
| 42 | 58 | 87.9 | 18 | 5 | AAE20857 Aae20857 E10-novis |
| 43 | 57 | 86.4 | 12 | 4 | AAB70664 Aab70664 Ovine SMA |
| 44 | 57 | 86.4 | 18 | 5 | AAE20872 Aae20872 E10-novis |
| 45 | 57 | 86.4 | 18 | 5 | AAE20873 Aae20873 DI10-novis |

ALIGNMENTS

RESULT 1
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ID AAB70661 standard; peptide; 14 AA.
XX
AC AAB70661;
XX
DT 15-MAY-2001 (first entry)
XX
DE Ovine SNAP 29 cathelicidin derived antimicrobial peptide SEQ ID NO:14.
XX
KW Ovine: SNAP29; lupine; RCP 18; cathelicidin; antimicrobial;
KW bactericidal; antibiotic; antiviral; microbial growth inhibitor;
KW proliferation inhibitor; gene therapy; Pseudomonas aeruginosa;
KW Burkholderia cepacia; Alcaligenes; Xanthomonas.
XX
OS Ovis aries.
XX
PN MO200112668-A1.
XX
PD 22-FEB-2001.
XX
PF 18-AUG-2000; 2000MO-US022781.
XX
PR 18-AUG-1999; 990US-0149886P.
XX
PA (IOWA) UNIV IOWA RES FOUND.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Tack BE, Mccray P, Welsh M, Travis SM, Lehrer R;
XX
DR WPI; 2001-234911/24.
XX
PT New antimicrobial peptides useful as antibiotics for inhibiting growth
XX and proliferation of microbes, and for treating microbial infections.
XX
PS Claim 1; Page 103; 137pp; English.
XX
CC AAB70648 to AAB70675 represent antimicrobial peptides (1), of which
CC AAB70648 to AAB70664, AAB70674 and AAB70675 are derived from the ovine
CC SNAP 29 cathelicidin family peptide, and AAB70665 to AAB70673 are derived
CC from the lupine RCP 18 cathelicidin family peptide. (1) have antibiotic,
CC antimicrobial and antiviral activities, and can be used as microbial
CC growth and proliferation inhibitors and in gene therapy. (1) are useful
CC for inhibiting microbial growth in an environment capable of sustaining
CC such growth, for inhibiting microbial growth or strain in a host, and
CC inhibiting the growth of drug-resistant microbial strains such as
CC Pseudomonas aeruginosa, Burkholderia cepacia, Alcaligenes and Xanthomonas

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:17:06 ; Search time 43.6816 Seconds

(without alignments)
164.122 Million cell updates/sec

Title: US-09-642-744d-13

Perfect score: 66

Sequence: 1 IRRIRKIHIIKK 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing:

Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|--------------|---------------------|
| 1 | 43 | 65.2 | 638 | 2 Q8D796 | Q8d796 vibrio vuln |
| 2 | 43 | 65.2 | 660 | 2 Q7MEAO | Q7meao vibrio vuln |
| 3 | 42 | 63.6 | 125 | 2 Q9AVZ1 | Q9avz1 guillardi |
| 4 | 42 | 63.6 | 308 | 2 Q8R2C7 | Q8r2c7 mus musculi |
| 5 | 42 | 63.6 | 414 | 2 Q94702 | Q94702 oryza sativ |
| 6 | 42 | 63.6 | 414 | 2 Q7XEY8 | Q7xey8 oryza sativ |
| 7 | 42 | 63.6 | 500 | 2 Q7X881 | Q7x881 achiliosacch |
| 8 | 42 | 63.6 | 500 | 2 Q7X881 | Q7x881 achiliosacch |
| 9 | 41 | 62.1 | 337 | 1 YBZ1 YEAST | YBZ1 yeas |
| 10 | 41 | 62.1 | 438 | 2 Q8TXS5 | Q8txs5 methanopyru |
| 11 | 41 | 62.1 | 613 | 1 DEAD_HAEIN | DEAD_HAEIN |
| 12 | 41 | 62.1 | 613 | 1 REP_BUCBP | REP_BUCBP |
| 13 | 41 | 62.1 | 1580 | 2 Q7RMP4 | Q7rmp4 plasmodium |
| 14 | 41 | 62.1 | 2084 | 2 Q8ILJ6 | Q8ilj6 plasmodium |
| 15 | 40 | 60.6 | 151 | 2 Q8R891 | Q8r891 thermococ |
| 16 | 40 | 60.6 | 160 | 1 SC51_SHEEP | SC51_SHEEP |
| 17 | 40 | 60.6 | 160 | 1 SC51_SHEEP | SC51_SHEEP |
| 18 | 40 | 60.6 | 240 | 2 Q7NSJ3 | Q7nsj3 photorhabd |
| 19 | 40 | 60.6 | 256 | 2 Q83CP2 | Q83cp2 coxiella bu |
| 20 | 40 | 60.6 | 328 | 2 Q72TV1 | Q72tv1 leptospira |
| 21 | 40 | 60.6 | 328 | 2 Q8F1B9 | Q8f1b9 leptospira |
| 22 | 40 | 60.6 | 370 | 2 Q67743 | Q67743 aquilex aeo |
| 23 | 40 | 60.6 | 452 | 2 Q7N787 | Q7n787 photorhabd |
| 24 | 40 | 60.6 | 475 | 2 Q7S6I8 | Q7s6i8 oryza sativ |
| 25 | 40 | 60.6 | 822 | 2 Q8C0U6 | Q8c0u6 methanosarc |
| 26 | 39 | 59.1 | 41 | 2 Q48971 | Q48971 pyrobaculum |
| 27 | 39 | 59.1 | 202 | 1 HANI_AQUAE | HANI_AQUAE |
| 28 | 39 | 59.1 | 210 | 2 Q92CL5 | Q92cl5 mycoplasma |
| 29 | 39 | 59.1 | 217 | 2 Q92CL5 | Q92cl5 mycoplasma |
| 30 | 39 | 59.1 | 217 | 2 Q92CL5 | Q92cl5 mycoplasma |
| 31 | 39 | 59.1 | 250 | 2 Q7W5F0 | Q7w5f0 bordetella |

| | | | | | |
|----|----|------|-----|--------------|--------------------|
| 32 | 39 | 59.1 | 250 | 2 Q7WCY5 | Q7wcy5 bordetella |
| 33 | 39 | 59.1 | 258 | 2 Q8MY71 | Q8my71 brachionus |
| 34 | 39 | 59.1 | 295 | 2 Q13635 | Q13635 schizosacch |
| 35 | 39 | 59.1 | 354 | 1 H1B1_OCEIH | H1B1_OCEIH |
| 36 | 39 | 59.1 | 407 | 2 Q9UTL1 | Q9utl1 oceanobacil |
| 37 | 39 | 59.1 | 415 | 2 Q9SPV4 | Q9spv4 schizosacch |
| 38 | 39 | 59.1 | 460 | 2 Q9VLO3 | Q9vlo3 nicotiana t |
| 39 | 39 | 59.1 | 461 | 2 Q8IBW2 | Q8ibw2 dirosophila |
| 40 | 39 | 59.1 | 483 | 2 Q9KR81 | Q9kr81 plasmodium |
| 41 | 39 | 59.1 | 549 | 2 Q8IPC2 | Q8ipc2 vibrio chol |
| 42 | 39 | 59.1 | 598 | 2 Q7VTH0 | Q7vth0 dirosophila |
| 43 | 39 | 59.1 | 647 | 2 Q6Z647 | Q6z647 bordetella |
| 44 | 39 | 59.1 | 834 | 2 Q6FW11 | Q6fw11 oryza sativ |
| 45 | 39 | 59.1 | 866 | 2 Q8JDJ9 | Q8jdj9 candida gla |

ALIGNMENTS

| RESULT 1 | ID | Q8D796 | PRELIMINARY; | PRT; | 638 AA. |
|-----------------------|---|--------------|---------------|------------|-------------|
| AC | Q8D796; | | | | |
| DT | 01-MAR-2003 (TREMBlrel. 23, Created) | | | | |
| DT | 01-MAR-2003 (TREMBlrel. 23, Last sequence update) | | | | |
| DE | 01-MAR-2004 (TREMBlrel. 26, Last annotation update) | | | | |
| DE | Predicted signal transduction protein. | | | | |
| OS | OrderedLocustNames=VV20264; | | | | |
| OC | Vibrio vulnificus. | | | | |
| OC | Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; | | | | |
| OC | Vibrionaceae; Vibrio. | | | | |
| OX | NCBI_TaxID=672; | | | | |
| RN | [1] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | STRATIN=CMCP6; | | | | |
| RA | Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H., | | | | |
| RA | Choy H.B.; | | | | |
| RT | "Complete genome sequence of Vibrio vulnificus CMCP6."; | | | | |
| RL | Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases. | | | | |
| DR | EMBL; AE016808; AAC07230.1; - | | | | |
| DR | InterPro; IPR001633; EAL. | | | | |
| DR | InterPro; IPR003018; GAF. | | | | |
| DR | InterPro; IPR000160; GDEF. | | | | |
| DR | Pfam; PF00563; EAL; 1. | | | | |
| DR | Pfam; PF01590; GAF; 1. | | | | |
| DR | Pfam; PF00990; GDEF; 1. | | | | |
| DR | SMART; SM00052; DUF2; 1. | | | | |
| DR | SMART; SM00065; GAF; 1. | | | | |
| DR | TIGRFAMs; TIGR00254; GDEF; 1. | | | | |
| DR | PROSITE; PS00883; EAL; 1. | | | | |
| DR | PROSITE; PS00887; GDEF; 1. | | | | |
| KW | Complete proteome. | | | | |
| SO | SEQUENCE 638 AA; 72187 MW; 7D13E28DF3A3F099 CRC64; | | | | |
| Query Match | | 65.2%; | Score 43; | DB 2; | Length 638; |
| Best Local Similarity | | 61.5%; | Pred. No. 62; | | |
| Matches | 8; | Conservative | 2; | Mismatches | 3; |
| | | | | Indels | 0; |
| | | | | Gaps | 0; |
| Qy | 2 RRIIRKIHIIKK 14 | | | | |
| Db | 566 KEIIRSIHVAKK 578 | | | | |
| RESULT 2 | | | | | |
| ID | Q7MEAO | PRELIMINARY; | PRT; | 660 AA. | |
| AC | Q7MEAO; | | | | |
| DT | 01-MAR-2004 (TREMBlrel. 26, Created) | | | | |
| DT | 01-MAR-2004 (TREMBlrel. 26, Last sequence update) | | | | |
| DE | 01-MAR-2004 (TREMBlrel. 26, Last annotation update) | | | | |
| DE | GGDEF family protein. | | | | |
| GN | OrderedLocustNames=VVA0770; | | | | |
| OS | Vibrio vulnificus (strain VJ016). | | | | |

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:21:40 / Search time 8.68156 Seconds

(without alignments)
155.160 Million cell updates/sec

Title: us-09-642-744d-13

Perfect score: 66

Sequence: 1 IRRIIRKIHIIKK 14

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|---------------------|
| 1 | 42 | 63.6 | 125 | 2 A99114 | hypothetical prote |
| 2 | 42 | 63.6 | 867 | 2 G69485 | DNA-directed RNA p |
| 3 | 41 | 62.1 | 337 | 2 S46010 | hypothetical prote |
| 4 | 41 | 62.1 | 613 | 2 F64056 | probable ATP-depen |
| 5 | 40 | 60.6 | 152 | 2 S68411 | catheлин-related p |
| 6 | 40 | 60.6 | 160 | 2 S68412 | myeloid antimicrob |
| 7 | 40 | 60.6 | 160 | 2 S68428 | GTP-binding protei |
| 8 | 40 | 60.6 | 370 | 2 C70464 | hypothetical prote |
| 9 | 39 | 59.1 | 41 | 2 S77768 | conserved hypotet |
| 10 | 39 | 59.1 | 202 | 1 H70318 | precortin isomeras |
| 11 | 39 | 59.1 | 210 | 2 AC1577 | hypothetical prote |
| 12 | 39 | 59.1 | 407 | 2 T37888 | hypothetical prote |
| 13 | 39 | 59.1 | 483 | 2 B82160 | spermatid protein |
| 14 | 38 | 57.6 | 87 | 2 S00180 | DNA-dependent RNA |
| 15 | 38 | 57.6 | 234 | 2 D97108 | sigk protein - Clo |
| 16 | 38 | 57.6 | 234 | 2 I40822 | transposase BME114 |
| 17 | 38 | 57.6 | 222 | 2 AB3430 | transposase BME114 |
| 18 | 38 | 57.6 | 623 | 2 S73432 | transposase BME114 |
| 19 | 38 | 57.6 | 623 | 2 S73432 | transposase BME114 |
| 20 | 37 | 56.1 | 62 | 1 R5B53F | heiliase (EC 3.6.1 |
| 21 | 37 | 56.1 | 212 | 2 A64045 | ribosomal protein |
| 22 | 37 | 56.1 | 284 | 2 A10897 | 2-dehydro-3-deoxy- |
| 23 | 37 | 56.1 | 303 | 2 F71212 | tagarose-bisphosph |
| 24 | 37 | 56.1 | 334 | 2 B72301 | hypothetical prote |
| 25 | 37 | 56.1 | 364 | 2 C70322 | endooglucanase - Th |
| 26 | 37 | 56.1 | 368 | 2 C69984 | conserved hypotet |
| 27 | 37 | 56.1 | 420 | 2 S45630 | DNA primase chain |
| 28 | 37 | 56.1 | 483 | 2 S75369 | hypothetical prote |
| 29 | 37 | 56.1 | 569 | 2 C83952 | prolyl-CRNA synthe |

| | | | | | |
|----|----|------|------|----------|--------------------|
| 30 | 37 | 56.1 | 813 | 2 T20527 | hypothetical prote |
| 31 | 37 | 56.1 | 856 | 1 VCLJ3W | env polyprotein pr |
| 32 | 36 | 54.5 | 67 | 2 B72248 | ribosomal protein |
| 33 | 36 | 54.5 | 102 | 2 AD1420 | PTS cellobiose-spe |
| 34 | 36 | 54.5 | 102 | 2 AE1795 | PTS cellobiose-spe |
| 35 | 36 | 54.5 | 117 | 2 T12722 | hypothetical prote |
| 36 | 36 | 54.5 | 239 | 2 G72307 | hypothetical prote |
| 37 | 36 | 54.5 | 310 | 2 A05034 | hypothetical prote |
| 38 | 36 | 54.5 | 370 | 2 A05034 | hypothetical prote |
| 39 | 36 | 54.5 | 447 | 2 F81678 | GTP-binding protei |
| 40 | 36 | 54.5 | 499 | 2 G84972 | leucyl aminopeptid |
| 41 | 36 | 54.5 | 627 | 2 C82418 | GDEF family prote |
| 42 | 36 | 54.5 | 760 | 2 T24521 | hypothetical prote |
| 43 | 36 | 54.5 | 780 | 2 AB1801 | amino-terminal dom |
| 44 | 36 | 54.5 | 849 | 2 A96592 | hypothetical prote |
| 45 | 36 | 54.5 | 1188 | 2 C71231 | hypothetical prote |

ALIGNMENTS

RESULT 1

A99114 hypothetical protein orf125 [imported] - Guillardia theta nucleomorph

C/Species: nucleomorph Guillardia theta

C/Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont

C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C/Accession: A99114

R/Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Re

Nature 410, 1091-1096, 2001

A/Title: The highly reduced genome of an enslaved algal nucleus.

A/Reference number: A99082; MUID:11323671; PMID:11323671

A/Accession: A99114

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1125 <DOU>

A/Cross-references: UNIPROT:Q9AVZ1; GB:AJ010592; NID:G12580762; PIDN:CAAC27080.1; GSPDB:

C/Genetics:

A/Gene: orf125

A/Map position: 2

A/Genome: nucleomorph

C/Keywords: nucleomorph

| Query Match | Score | DB 2 | Length | 125 |
|-----------------------|-------|---------------|--------|------------|
| Best Local Similarity | 70.0% | Pred. No. 6.6 | | |
| Matches | 7 | Conservative | 3 | Mismatches |
| | | | 0 | Indels |
| | | | 0 | Gaps |
| | | | 0 | |

| | | |
|----|---|------------|
| QY | 5 | IRRIIRK 14 |
| DB | 9 | IRRIIRK 18 |

RESULT 2

G69485 DNA-directed RNA polymerase, subunit A' (rpoA1) homolog - Archaeoglobus fulgidus

C/Species: Archaeoglobus fulgidus

C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

C/Accession: G69485

R/Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodac

., Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.;

Nature 390, 364-370, 1997

A/Authors: Uettermann, T.; Cotton, M.D.; Spriggs, T.; Artach, P.; Kahne, B.P.; Sykes, S

Smith, H.O.; Moese, C.R.; Venter, J.C.

A/Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae

A/Reference number: A69250; MUID:98049343; PMID:9389475

A/Accession: G69485

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-867 <KLB>

A/Cross-references: UNIPROT:Q028391; GB:AB000972; GB:AB000782; NID:G2689295; PIDN:AA8893

C/Superfamily: Halobacterium DNA-directed RNA polymerase chain A

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OM protein - protein search, using SW model

Run on: May 2, 2005, 13:03:56 ; Search time 38.0894 Seconds

(without alignments)
122.435 Million cell updates/sec

Title: US-09-642-744d-13

Perfect score: 66

Sequence: 1 IRRIRKIHITIKK 14

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1426032 seqs, 33106140 residues

Total number of hits satisfying chosen parameters: 1426032

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

1: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubppaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubppaa/US06_PUBCOMB.pep.*
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7: /cgn2_6/ptodata/1/pubppaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep.*
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19: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|------------------|-------------------|
| 1 | 66 | 100.0 | 14 | US-10-060-102-19 | Sequence 19, Appl |
| 2 | 66 | 100.0 | 14 | US-10-060-102-20 | Sequence 20, Appl |
| 3 | 66 | 100.0 | 14 | US-10-721-839-19 | Sequence 19, Appl |
| 4 | 66 | 100.0 | 14 | US-10-721-839-20 | Sequence 20, Appl |
| 5 | 66 | 100.0 | 14 | US-10-060-102-15 | Sequence 15, Appl |
| 6 | 66 | 100.0 | 14 | US-10-721-839-15 | Sequence 15, Appl |
| 7 | 66 | 100.0 | 14 | US-10-060-102-10 | Sequence 10, Appl |
| 8 | 66 | 100.0 | 14 | US-10-060-102-11 | Sequence 11, Appl |
| 9 | 66 | 100.0 | 14 | US-10-721-839-10 | Sequence 10, Appl |
| 10 | 66 | 100.0 | 14 | US-10-721-839-11 | Sequence 11, Appl |
| 11 | 64 | 97.0 | 14 | US-10-060-102-13 | Sequence 13, Appl |
| 12 | 64 | 97.0 | 14 | US-10-060-102-18 | Sequence 18, Appl |
| 13 | 64 | 97.0 | 14 | US-10-721-839-13 | Sequence 13, Appl |

| | | | | | |
|----|----|------|----|------------------|-------------------|
| 14 | 64 | 97.0 | 14 | US-10-721-839-18 | Sequence 18, Appl |
| 15 | 64 | 97.0 | 15 | US-10-060-102-14 | Sequence 14, Appl |
| 16 | 64 | 97.0 | 15 | US-10-721-839-14 | Sequence 14, Appl |
| 17 | 64 | 97.0 | 18 | US-09-840-009-2 | Sequence 2, Appl |
| 18 | 64 | 97.0 | 18 | US-09-840-009-9 | Sequence 9, Appl |
| 19 | 64 | 97.0 | 18 | US-09-840-009-16 | Sequence 16, Appl |
| 20 | 64 | 97.0 | 18 | US-09-840-009-23 | Sequence 23, Appl |
| 21 | 64 | 97.0 | 18 | US-09-840-009-30 | Sequence 30, Appl |
| 22 | 64 | 97.0 | 18 | US-10-060-102-9 | Sequence 9, Appl |
| 23 | 64 | 97.0 | 18 | US-10-060-102-12 | Sequence 12, Appl |
| 24 | 64 | 97.0 | 18 | US-10-721-839-9 | Sequence 9, Appl |
| 25 | 64 | 97.0 | 18 | US-10-721-839-12 | Sequence 12, Appl |
| 26 | 64 | 97.0 | 29 | US-10-060-102-8 | Sequence 8, Appl |
| 27 | 64 | 97.0 | 29 | US-10-721-839-8 | Sequence 8, Appl |
| 28 | 59 | 89.4 | 18 | US-09-840-009-4 | Sequence 4, Appl |
| 29 | 59 | 89.4 | 18 | US-09-840-009-8 | Sequence 8, Appl |
| 30 | 59 | 89.4 | 18 | US-09-840-009-11 | Sequence 11, Appl |
| 31 | 59 | 89.4 | 18 | US-09-840-009-15 | Sequence 15, Appl |
| 32 | 59 | 89.4 | 18 | US-09-840-009-18 | Sequence 18, Appl |
| 33 | 59 | 89.4 | 18 | US-09-840-009-22 | Sequence 22, Appl |
| 34 | 59 | 89.4 | 18 | US-09-840-009-25 | Sequence 25, Appl |
| 35 | 59 | 89.4 | 18 | US-09-840-009-29 | Sequence 29, Appl |
| 36 | 59 | 89.4 | 18 | US-10-060-102-25 | Sequence 25, Appl |
| 37 | 59 | 89.4 | 18 | US-10-721-839-25 | Sequence 25, Appl |
| 38 | 58 | 87.9 | 18 | US-09-840-009-5 | Sequence 5, Appl |
| 39 | 58 | 87.9 | 18 | US-09-840-009-12 | Sequence 12, Appl |
| 40 | 58 | 87.9 | 18 | US-09-840-009-19 | Sequence 19, Appl |
| 41 | 58 | 87.9 | 18 | US-09-840-009-26 | Sequence 26, Appl |
| 42 | 57 | 86.4 | 18 | US-09-840-009-6 | Sequence 6, Appl |
| 43 | 57 | 86.4 | 18 | US-09-840-009-7 | Sequence 7, Appl |
| 44 | 57 | 86.4 | 18 | US-09-840-009-13 | Sequence 13, Appl |
| 45 | 57 | 86.4 | 9 | US-09-840-009-14 | Sequence 14, Appl |

ALIGNMENTS

RESULT 1

US-10-060-102-19

Sequence 19, Application US/10060102

Publication No. US2003022829A1

GENERAL INFORMATION:

APPLICANT: MAURY, WENDY

APPLICANT: STRAPLETON, JACK

APPLICANT: ROLLER, RICHARD

APPLICANT: STINSKI, MARK

APPLICANT: MCCRAY, PAUL B.

APPLICANT: TACK, BRIAN

TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIVATE THETA DEFENSINS AND MAMMAL

TITLE OF INVENTION: CATHELICIDINS

FILE REFERENCE: IOWA.035US

CURRENT APPLICATION NUMBER: US/10/060,102

CURRENT FILING DATE: 2002-02-22

PRIOR APPLICATION NUMBER: 60/309,368

PRIOR FILING DATE: 2001-08-01

PRIOR APPLICATION NUMBER: 60/265,270

PRIOR FILING DATE: 2001-01-30

NUMBER OF SEQ ID NOS: 32

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 19

LENGTH: 14

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

OTHER INFORMATION: Peptide

US-10-060-102-19

Query Match 100.0%; Score 66; DB 14; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00056;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 IRRIRKIHITIKK 14

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 2, 2005, 12:18:40 ; Search time 13.2961 Seconds

(without alignments)
78.601 Million cell updates/sec

Title: US-09-642-744D-13
Perfect score: 66
Sequence: 1 IRRIRKIHIIKK 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/prodata/1/aa/5A COMB pep:.*
2: /cgn2_6/prodata/1/aa/5B COMB pep:.*
3: /cgn2_6/prodata/1/aa/6A COMB pep:.*
4: /cgn2_6/prodata/1/aa/6B COMB pep:.*
5: /cgn2_6/prodata/1/aa/6C COMB pep:.*
6: /cgn2_6/prodata/1/aa/6D COMB pep:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|------------------|
| 1 | 64 | 97.0 | 18 | 4 | US-09-840-009-2 |
| 2 | 64 | 97.0 | 18 | 4 | US-09-840-009-9 |
| 3 | 64 | 97.0 | 18 | 4 | US-09-840-009-16 |
| 4 | 64 | 97.0 | 18 | 4 | US-09-840-009-23 |
| 5 | 64 | 97.0 | 18 | 4 | US-09-840-009-30 |
| 6 | 59 | 89.4 | 18 | 4 | US-09-840-009-4 |
| 7 | 59 | 89.4 | 18 | 4 | US-09-840-009-8 |
| 8 | 59 | 89.4 | 18 | 4 | US-09-840-009-11 |
| 9 | 59 | 89.4 | 18 | 4 | US-09-840-009-15 |
| 10 | 59 | 89.4 | 18 | 4 | US-09-840-009-18 |
| 11 | 59 | 89.4 | 18 | 4 | US-09-840-009-22 |
| 12 | 59 | 89.4 | 18 | 4 | US-09-840-009-25 |
| 13 | 59 | 89.4 | 18 | 4 | US-09-840-009-29 |
| 14 | 58 | 87.9 | 18 | 4 | US-09-840-009-5 |
| 15 | 58 | 87.9 | 18 | 4 | US-09-840-009-12 |
| 16 | 58 | 87.9 | 18 | 4 | US-09-840-009-19 |
| 17 | 58 | 87.9 | 18 | 4 | US-09-840-009-26 |
| 18 | 57 | 86.4 | 18 | 4 | US-09-840-009-6 |
| 19 | 57 | 86.4 | 18 | 4 | US-09-840-009-7 |
| 20 | 57 | 86.4 | 18 | 4 | US-09-840-009-13 |
| 21 | 57 | 86.4 | 18 | 4 | US-09-840-009-14 |
| 22 | 57 | 86.4 | 18 | 4 | US-09-840-009-20 |
| 23 | 57 | 86.4 | 18 | 4 | US-09-840-009-21 |
| 24 | 57 | 86.4 | 18 | 4 | US-09-840-009-27 |
| 25 | 57 | 86.4 | 18 | 4 | US-09-840-009-28 |
| 26 | 56 | 84.8 | 18 | 4 | US-09-840-009-3 |
| 27 | 56 | 84.8 | 18 | 4 | US-09-840-009-10 |

| | | | | | | |
|----|----|------|-----|---|---------------------|-------------------|
| 28 | 56 | 84.8 | 18 | 4 | US-09-840-009-17 | Sequence 17, Appl |
| 29 | 56 | 84.8 | 18 | 4 | US-09-840-009-24 | Sequence 24, Appl |
| 30 | 56 | 84.8 | 18 | 4 | US-09-840-009-31 | Sequence 31, Appl |
| 31 | 56 | 84.8 | 18 | 4 | US-09-840-009-34 | Sequence 34, Appl |
| 32 | 56 | 84.8 | 18 | 4 | US-09-840-009-35 | Sequence 35, Appl |
| 33 | 48 | 72.7 | 18 | 4 | US-09-840-009-32 | Sequence 32, Appl |
| 34 | 48 | 72.7 | 18 | 4 | US-09-840-009-33 | Sequence 33, Appl |
| 35 | 48 | 72.7 | 18 | 4 | US-09-840-009-36 | Sequence 36, Appl |
| 36 | 48 | 72.7 | 18 | 4 | US-09-840-009-37 | Sequence 37, Appl |
| 37 | 44 | 66.7 | 18 | 4 | US-09-840-009-1 | Sequence 1, Appl |
| 38 | 42 | 63.6 | 24 | 4 | US-09-785-0598-5 | Sequence 5, Appl |
| 39 | 42 | 63.6 | 36 | 4 | US-09-785-0598-6 | Sequence 6, Appl |
| 40 | 42 | 63.6 | 42 | 4 | US-09-785-0598-7 | Sequence 7, Appl |
| 41 | 42 | 62.1 | 48 | 4 | US-09-785-0598-8 | Sequence 8, Appl |
| 42 | 41 | 62.1 | 337 | 4 | US-09-538-092-38 | Sequence 38, Appl |
| 43 | 41 | 62.1 | 391 | 3 | US-09-134-001C-5234 | Sequence 5234, Ap |
| 44 | 40 | 60.6 | 160 | 4 | US-09-917-340-35 | Sequence 35, Appl |
| 45 | 40 | 60.6 | 169 | 4 | US-09-270-767-35406 | Sequence 35406, A |

ALIGNMENTS

```
RESULT 1
US-09-840-009-2
; Sequence 2, Application US/09840009
; Patent No. 6492328
; GENERAL INFORMATION:
; APPLICANT: Lehner, Robert I.
; APPLICANT: Waring, Alan J.
; APPLICANT: Tack, Brian F.
; TITLE OF INVENTION: NOVISPRINS: ANTIMICROBIAL PEPTIDES
; FILE REFERENCE: 06510-195MO
; CURRENT APPLICATION NUMBER: US/09/840,009
; PRIOR FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 09/606,858
; PRIOR FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic antimicrobial peptide
US-09-840-009-2
Query Match          97.0%  Score 64;  DB 4;  Length 18;
Best Local Similarity 92.9%  Pred. No. 0.00098;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY      1 IRRIRKIHIIKK 14
DB      3 LRRIRKIHIIKK 16
RESULT 2
US-09-840-009-9
; Sequence 9, Application US/09840009
; Patent No. 6492328
; GENERAL INFORMATION:
; APPLICANT: Lehner, Robert I.
; APPLICANT: Waring, Alan J.
; APPLICANT: Tack, Brian F.
; TITLE OF INVENTION: NOVISPRINS: ANTIMICROBIAL PEPTIDES
; FILE REFERENCE: 06510-195MO
; CURRENT APPLICATION NUMBER: US/09/840,009
; PRIOR FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 09/606,858
; PRIOR FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:17:55 ; Search time 49.0782 Seconds

(without alignments)
110.327 Million cell updates/sec

Title: US-09-642-744d-13

Perfect score: 66

Sequence: 1 IRRIRKIRIRIKK 14

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_16Dec04:*
1: geneseqp19808:*
2: geneseqp19908:*
3: geneseqp20008:*
4: geneseqp20018:*
5: geneseqp20028:*
6: geneseqp20038:*
7: geneseqp20048:*
8: geneseqp20058:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|------------|--------------------|
| 1 | 66 | 100.0 | 14 | 4 AAB70661 | Aab70661 Ovine SMA |
| 2 | 66 | 100.0 | 14 | 4 AAB70660 | Aab70660 Ovine SMA |
| 3 | 66 | 100.0 | 14 | 5 ABP53286 | ABP53286 Synthetic |
| 4 | 66 | 100.0 | 14 | 5 ABP53287 | ABP53287 Synthetic |
| 5 | 66 | 100.0 | 16 | 4 AAB70657 | Aab70657 Ovine SMA |
| 6 | 66 | 100.0 | 16 | 5 ABP53282 | ABP53282 Synthetic |
| 7 | 66 | 100.0 | 18 | 4 AAB70654 | Aab70654 Ovine SMA |
| 8 | 66 | 100.0 | 18 | 5 ABP53278 | ABP53278 Synthetic |
| 9 | 66 | 100.0 | 18 | 5 ABP53277 | ABP53277 Synthetic |
| 10 | 64 | 97.0 | 20 | 4 AAB70653 | Aab70653 Ovine SMA |
| 11 | 64 | 97.0 | 14 | 4 AAB70658 | Aab70658 Ovine SMA |
| 12 | 64 | 97.0 | 14 | 4 AAB70659 | Aab70659 Ovine SMA |
| 13 | 64 | 97.0 | 14 | 5 ABP53280 | ABP53280 Synthetic |
| 14 | 64 | 97.0 | 14 | 5 ABP53285 | ABP53285 Synthetic |
| 15 | 64 | 97.0 | 16 | 4 AAB70656 | Aab70656 Ovine SMA |
| 16 | 64 | 97.0 | 18 | 5 ABP53281 | ABP53281 Synthetic |
| 17 | 64 | 97.0 | 18 | 4 AAB70655 | Aab70655 Ovine SMA |
| 18 | 64 | 97.0 | 18 | 4 AAB70648 | Aab70648 Ovine SMA |
| 19 | 64 | 97.0 | 18 | 5 AAE20882 | AAE20882 Synthetic |
| 20 | 64 | 97.0 | 18 | 5 AAE20875 | AAE20875 Synthetic |
| 21 | 64 | 97.0 | 18 | 5 AAE20854 | AAE20854 Synthetic |
| 22 | 64 | 97.0 | 18 | 5 AAE20861 | AAE20861 Synthetic |
| 23 | 64 | 97.0 | 18 | 5 AAE20868 | AAE20868 Synthetic |
| 24 | 64 | 97.0 | 18 | 5 ABP53276 | ABP53276 Synthetic |
| 25 | 64 | 97.0 | 18 | 5 ABP53279 | ABP53279 Synthetic |

| | | | | | |
|----|----|------|----|------------|--------------------|
| 26 | 64 | 97.0 | 29 | 4 AAB70675 | Aab70675 Ovine SMA |
| 27 | 64 | 97.0 | 29 | 5 ABP53275 | ABP53275 Synthetic |
| 28 | 62 | 93.9 | 13 | 4 AAB70663 | Aab70663 Ovine SMA |
| 29 | 59 | 89.4 | 13 | 4 AAB70662 | Aab70662 Ovine SMA |
| 30 | 59 | 89.4 | 18 | 5 AAE20870 | AAE20870 Synthetic |
| 31 | 59 | 89.4 | 18 | 5 AAE20860 | AAE20860 Synthetic |
| 32 | 59 | 89.4 | 18 | 5 AAE20881 | AAE20881 Synthetic |
| 33 | 59 | 89.4 | 18 | 5 AAE20867 | AAE20867 Synthetic |
| 34 | 59 | 89.4 | 18 | 5 AAE20874 | AAE20874 Synthetic |
| 35 | 59 | 89.4 | 18 | 5 AAE20863 | AAE20863 Synthetic |
| 36 | 59 | 89.4 | 18 | 5 AAE20877 | AAE20877 Synthetic |
| 37 | 59 | 89.4 | 18 | 5 AAE20856 | AAE20856 Synthetic |
| 38 | 59 | 89.4 | 18 | 5 ABP53292 | ABP53292 Synthetic |
| 39 | 58 | 87.9 | 18 | 5 AAE20864 | AAE20864 Synthetic |
| 40 | 58 | 87.9 | 18 | 5 AAE20871 | AAE20871 Synthetic |
| 41 | 58 | 87.9 | 18 | 5 AAE20878 | AAE20878 Synthetic |
| 42 | 58 | 87.9 | 18 | 5 AAE20857 | AAE20857 Synthetic |
| 43 | 57 | 86.4 | 12 | 4 AAB70664 | Aab70664 Ovine SMA |
| 44 | 57 | 86.4 | 18 | 5 AAE20872 | AAE20872 Synthetic |
| 45 | 57 | 86.4 | 18 | 5 AAE20873 | AAE20873 Synthetic |

ALIGNMENTS

RESULT 1
AAB70661
ID AAB70661 standard; peptide; 14 AA.
XX
AC AAB70661;
XX
DT 15-MAY-2001 (first entry)
XX
DE Ovine SNAP 29 cathelicidin derived antimicrobial peptide SEQ ID NO:14.
XX
XX Ovine; SNAP29; lupine; RCAP 18; cathelicidin; antimicrobial;
XX bacterial; antibiotic; antiviral; microbial growth inhibitor;
XX proliferation inhibitor; gene therapy; Pseudomonas aeruginosa;
XX Burkholderia cepacia; Alcaligenes; Xanthomonas.
XX
XX Ovis aries.
XX
XX WO200112668-A1.
XX
XX 22-FEB-2001.
XX
XX 18-AUG-2000; 2000MO-US022781.
XX
XX 18-AUG-1999; 99US-0149886P.
XX
XX (IOWA) UNIV IOWA RES FOUND.
XX (REGC) UNIV CALIFORNIA.
XX
XX Tick BE, Mccray P, Welsh M, Travis SM, Lehrer R,
XX WPI; 2001-234911/24.
XX
XX New antimicrobial peptides useful as antibiotics for inhibiting growth
XX and proliferation of microbes, and for treating microbial infections.
XX
XX Claim 1; Page 103; 137pp; English.
XX
XX AAB70648 to AAB70675 represent antimicrobial peptides (I), of which
XX AAB70648 to AAB70664, AAB70674 and AAB70675 are derived from the ovine
XX SNAP 29 cathelicidin family peptide, and AAB70665 to AAB70673 are derived
XX from the lupine RCAP 18 cathelicidin family peptide. (I) have antibiotic,
XX antimicrobial and antiviral activities, and can be used as microbial
XX growth and proliferation inhibitors and in gene therapy. (II) are useful
XX for inhibiting microbial growth in an environment capable of sustaining
XX such growth, for inhibiting microbial growth or strain in a host, and
XX inhibiting the growth of drug-resistant microbial strains such as
XX Pseudomonas aeruginosa, Burkholderia cepacia, Alcaligenes and Xanthomonas

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:17:06 / Search time 43.6816 Seconds

(without alignments)
164.122 Million cell updates/sec

Title: US-09-642-744D-12

Perfect score: 66

Sequence: 1 LRRIKIHVAKK 14

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: UniProt 03:
1: uniprot_sprot:
2: uniprot_trembl:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 43 | 65.2 | 638 | 2 | Q8D796 |
| 2 | 43 | 65.2 | 660 | 2 | Q7MEAO |
| 3 | 42 | 63.6 | 125 | 2 | Q9AVZ1 |
| 4 | 42 | 63.6 | 160 | 1 | SC51_SHEEP |
| 5 | 42 | 63.6 | 160 | 1 | SC52_SHEEP |
| 6 | 42 | 63.6 | 308 | 2 | Q8R2C7 |
| 7 | 42 | 63.6 | 500 | 1 | TF3B_SCHRO |
| 8 | 41 | 62.1 | 41 | 2 | Q48971 |
| 9 | 41 | 62.1 | 217 | 1 | Q977R2 |
| 10 | 41 | 62.1 | 337 | 1 | YBZ1_YEAST |
| 11 | 41 | 62.1 | 414 | 2 | Q94702 |
| 12 | 41 | 62.1 | 613 | 1 | Q7XEY8 |
| 13 | 41 | 62.1 | 613 | 1 | DEAD_HAEN |
| 14 | 41 | 62.1 | 670 | 1 | REP_BUCBP |
| 15 | 40 | 60.6 | 256 | 2 | Q83CP2 |
| 16 | 40 | 60.6 | 370 | 2 | Q67743 |
| 17 | 40 | 60.6 | 452 | 2 | Q7N787 |
| 18 | 40 | 60.6 | 461 | 2 | Q81BM2 |
| 19 | 40 | 60.6 | 475 | 2 | Q7SGI8 |
| 20 | 40 | 60.6 | 867 | 2 | Q28391 |
| 21 | 39 | 59.1 | 202 | 1 | HAML_AQUAE |
| 22 | 39 | 59.1 | 210 | 2 | Q92CT5 |
| 23 | 39 | 59.1 | 250 | 2 | Q7W5F0 |
| 24 | 39 | 59.1 | 250 | 2 | Q7W5F0 |
| 25 | 39 | 59.1 | 258 | 2 | Q8MY71 |
| 26 | 39 | 59.1 | 349 | 2 | Q736D5 |
| 27 | 39 | 59.1 | 349 | 2 | Q81P89 |
| 28 | 39 | 59.1 | 349 | 2 | Q6H112 |
| 29 | 39 | 59.1 | 407 | 2 | Q9UTH1 |
| 30 | 39 | 59.1 | 428 | 2 | Q8TXS5 |
| 31 | 39 | 59.1 | 483 | 2 | Q9KR81 |

| | | | | | | |
|----|----|------|------|---|------------|------------|
| 32 | 39 | 59.1 | 598 | 2 | Q7VTH0 | Q7VTH0 |
| 33 | 39 | 59.1 | 838 | 2 | Q9DVL4 | Q9DVL4 |
| 34 | 39 | 59.1 | 903 | 2 | Q95WA7 | Q95WA7 |
| 35 | 39 | 59.1 | 967 | 2 | Q7RJB4 | Q7RJB4 |
| 36 | 39 | 59.1 | 1157 | 2 | Q7RONS | Q7RONS |
| 37 | 39 | 59.1 | 1160 | 2 | Q7SBL3 | Q7SBL3 |
| 38 | 39 | 59.1 | 1226 | 2 | Q6L573 | Q6L573 |
| 39 | 39 | 59.1 | 1580 | 2 | Q7RMP4 | Q7RMP4 |
| 40 | 39 | 59.1 | 2084 | 2 | Q81J6 | Q81J6 |
| 41 | 39 | 59.1 | 4057 | 2 | Q81J67 | Q81J67 |
| 42 | 38 | 57.6 | 87 | 1 | SSS1_SCYCA | SSS1_SCYCA |
| 43 | 38 | 57.6 | 102 | 2 | Q8Y3R8 | Q8Y3R8 |
| 44 | 38 | 57.6 | 102 | 2 | Q926Y2 | Q926Y2 |
| 45 | 38 | 57.6 | 102 | 2 | Q71VZ6 | Q71VZ6 |

ALIGNMENTS

| RESULT 1 | ID | Q8D796 | PRELIMINARY: | PRT: | 638 AA. |
|-----------------------|---|--------------------------------------|---------------|------------|-------------|
| AC | Q8D796 | 01-MAR-2003 (TREMBLrel. 23, Created) | | | |
| DT | 01-MAR-2003 (TREMBLrel. 23, Last sequence update) | | | | |
| DE | 01-MAR-2004 (TREMBLrel. 26, Last annotation update) | | | | |
| GN | OrderedLocustNames=VV20264; | | | | |
| OS | Vibrio vulnificus. | | | | |
| OC | Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; | | | | |
| OX | Vibrionaceae; Vibrio. | | | | |
| NCBI_TaxID=672; | | | | | |
| SEQUENCE FROM N.A. | | | | | |
| RA | Rhe H.E.; | | | | |
| RT | "Complete genome sequence of Vibrio vulnificus CMCP6." | | | | |
| RL | Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases. | | | | |
| DR | EMBL; AE016808; AAC07230.1; - | | | | |
| DR | InterPro; IPR001633; EAL. | | | | |
| DR | InterPro; IPR003018; GAF. | | | | |
| DR | InterPro; IPR00160; GDEF. | | | | |
| DR | Pfam; PF00563; EAL; 1. | | | | |
| DR | Pfam; PF01590; GAF; 1. | | | | |
| DR | Pfam; PF00990; GDEF; 1. | | | | |
| DR | SMART; SM00052; DUF2; 1. | | | | |
| DR | SMART; SM00065; GAF; 1. | | | | |
| DR | TIGRFAMs; TIGR00254; GDEF; 1. | | | | |
| DR | PROSITE; PSS0883; EAL; 1. | | | | |
| KW | Complete proteome. | | | | |
| SO | SEQUENCE 638 AA; 72187 MW; 7D13E2BDF3A3F099 CRC64; | | | | |
| Query Match | | 65.2%; | Score 43; | DB 2; | Length 638; |
| Best Local Similarity | | 61.5%; | Pred. No. 65; | | |
| Matches | 8; | Conservative | 2; | Mismatches | 3; |
| Indels | 0; | Gaps | 0; | | |
| Db | 2 LRRIKIHVAKK 14 | | | | |
| 566 | KEIRSIHVAKK 578 | | | | |
| RESULT 2 | | | | | |
| Q7MEAO | | | | | |
| AC | Q7MEAO | PRELIMINARY: | PRT: | 660 AA. | |
| DT | 01-MAR-2004 (TREMBLrel. 26, Created) | | | | |
| DT | 01-MAR-2004 (TREMBLrel. 26, Last sequence update) | | | | |
| DE | 01-MAR-2004 (TREMBLrel. 26, Last annotation update) | | | | |
| GN | OrderedLocustNames=VVA0770; | | | | |
| OS | Vibrio vulnificus (strain V016). | | | | |

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:21:40 ; Search time 8.68156 Seconds

(Without alignment)
155.160 Million cell updates/sec

Title: US-09-642-744D-12

Sequence: 1 LRRIKIHITK 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: PIR 79:*

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 42 | 63.6 | 125 | 2 | A99114 |
| 2 | 42 | 63.6 | 152 | 2 | S68411 |
| 3 | 42 | 63.6 | 160 | 2 | S68412 |
| 4 | 42 | 63.6 | 160 | 2 | S68228 |
| 5 | 41 | 62.1 | 41 | 2 | S77768 |
| 6 | 41 | 62.1 | 337 | 2 | S46010 |
| 7 | 41 | 62.1 | 613 | 2 | F64056 |
| 8 | 40 | 60.6 | 370 | 2 | C70464 |
| 9 | 40 | 60.6 | 867 | 2 | G69485 |
| 10 | 39 | 59.1 | 202 | 1 | H70318 |
| 11 | 39 | 59.1 | 210 | 2 | AC1577 |
| 12 | 39 | 59.1 | 407 | 2 | T17888 |
| 13 | 39 | 59.1 | 483 | 2 | B82160 |
| 14 | 38 | 57.6 | 87 | 2 | S00180 |
| 15 | 38 | 57.6 | 102 | 2 | AD1420 |
| 16 | 38 | 57.6 | 102 | 2 | AB1795 |
| 17 | 38 | 57.6 | 272 | 2 | AB3430 |
| 18 | 38 | 57.6 | 284 | 2 | AT0897 |
| 19 | 38 | 57.6 | 623 | 2 | S73462 |
| 20 | 38 | 57.6 | 698 | 2 | D64084 |
| 21 | 38 | 57.6 | 780 | 2 | AB1801 |
| 22 | 38 | 57.6 | 1188 | 2 | C71231 |
| 23 | 37 | 56.1 | 334 | 2 | B72301 |
| 24 | 37 | 56.1 | 352 | 2 | H86454 |
| 25 | 37 | 56.1 | 368 | 2 | C69484 |
| 26 | 37 | 56.1 | 569 | 2 | C63952 |
| 27 | 37 | 56.1 | 594 | 2 | D70127 |
| 28 | 36 | 54.5 | 117 | 2 | T12722 |
| 29 | 36 | 54.5 | 234 | 2 | D97108 |

| | | | | | | |
|----|----|------|------|---|--------|----------------------|
| 30 | 36 | 54.5 | 234 | 2 | I40822 | sigk protein - C10 |
| 31 | 36 | 54.5 | 299 | 2 | G72307 | hypothetical prote |
| 32 | 36 | 54.5 | 310 | 2 | A33489 | hypothetical prote |
| 33 | 36 | 54.5 | 357 | 2 | S21992 | envelope protein 9 |
| 34 | 36 | 54.5 | 370 | 2 | A05034 | hypothetical prote |
| 35 | 36 | 54.5 | 447 | 2 | F81678 | GTP-binding protei |
| 36 | 36 | 54.5 | 484 | 2 | A70558 | hypothetical prote |
| 37 | 36 | 54.5 | 499 | 2 | G84972 | leucyl aminopeptid |
| 38 | 36 | 54.5 | 627 | 2 | C82418 | GDH family prote |
| 39 | 36 | 54.5 | 672 | 2 | S46276 | acetate-CoA ligase |
| 40 | 36 | 54.5 | 760 | 2 | T24521 | hypothetical prote |
| 41 | 36 | 54.5 | 780 | 2 | AC1427 | transcriptional regu |
| 42 | 36 | 54.5 | 1014 | 2 | T30840 | serine-repeat anti |
| 43 | 36 | 54.5 | 8243 | 2 | T31307 | type I fatty acid |
| 44 | 35 | 53.0 | 62 | 1 | R5H31F | ribosomal protein |
| 45 | 35 | 53.0 | 98 | 2 | T22503 | hypothetical prote |

ALIGNMENTS

RESULT 1

A99114
hypothetical protein orf125 [imported] - Giardia theta nucleomorph

C:Species: nucleomorph Giardia theta

A:Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont

C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C:Accession: A99114
R:Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Re

Nature 410, 1091-1096, 2001
A:Title: The highly reduced genome of an enslaved algal nucleus.

A:Reference number: A99082; PMID:11323671, PMID:11323671

A:Accession: A99114
A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-125 <DOU>

A:Cross-references: UNIPROT:Q9AVZ1; GB:A010592; NID:g12580762; PIDN:CAC27080.1; GSPDB:

C:Genetics:
A:Gene: orf125

A:Map position: 2
A:Genome: nucleomorph

C:Keywords: nucleomorph

Query Match 63.6%; Score 42; DB 2; Length 125;
Best Local Similarity 70.0%; Pred. No. 7;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 5 IRKIHITK 14
DB 9 IRKIHITK 18

RESULT 2

S68411
cathelin-related protein 2 precursor - sheep (fragment)

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000

C:Accession: S68411
R:Mahoney, M.M.; Lee, A.Y.; Brezinski-Calguri, D.J.; Huttner, K.M.

FEBS Lett. 377, 519-522, 1995
A:Title: Molecular analysis of the sheep cathelin family reveals a novel antimicrobial

A:Reference number: S68411; PMID:8549789

A:Accession: S68411
A:Status: preliminary

A:Molecule type: mRNA
A:Residues: 1-152 <MAH>

A:Cross-references: EMBL:X92757
C:Genetics:

A:Gene: SCS-2
C:Superfamily: cathelin; cystatin homology

F:1-21/Domain: signal sequence #stratus predicted <SIG>
F:21-123/Domain: cystatin homology <CTS>
F:21-123/Domain: propeptide #stratus predicted <PRO>

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 2, 2005, 13:03:56 ; Search time 38.0894 Seconds
(without alignments)
122.435 Million cell updates/sec

Title: US-09-642-744d-12

Perfect score: 66
Sequence: 1 LRRIRKIIHIYK 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1426032 seqs, 333106140 residues

Total number of hits satisfying chosen parameters: 1426032

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
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- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|------------------|-------------------|
| 1 | 66 | 100.0 | 14 | US-10-060-102-13 | Sequence 13, Appl |
| 2 | 66 | 100.0 | 14 | US-10-060-102-18 | Sequence 18, Appl |
| 3 | 66 | 100.0 | 14 | US-10-721-839-13 | Sequence 13, Appl |
| 4 | 66 | 100.0 | 14 | US-10-721-839-18 | Sequence 18, Appl |
| 5 | 66 | 100.0 | 16 | US-10-060-102-14 | Sequence 14, Appl |
| 6 | 66 | 100.0 | 16 | US-10-721-839-14 | Sequence 14, Appl |
| 7 | 66 | 100.0 | 18 | US-09-840-009-2 | Sequence 2, Appl |
| 8 | 66 | 100.0 | 18 | US-09-840-009-9 | Sequence 9, Appl |
| 9 | 66 | 100.0 | 18 | US-09-840-009-16 | Sequence 16, Appl |
| 10 | 66 | 100.0 | 18 | US-09-840-009-23 | Sequence 23, Appl |
| 11 | 66 | 100.0 | 18 | US-09-840-009-30 | Sequence 30, Appl |
| 12 | 66 | 100.0 | 18 | US-10-060-102-9 | Sequence 9, Appl |
| 13 | 66 | 100.0 | 18 | US-10-060-102-12 | Sequence 12, Appl |

| | | | | | |
|----|----|-------|----|------------------|-------------------|
| 14 | 66 | 100.0 | 18 | US-10-721-839-9 | Sequence 9, Appl |
| 15 | 66 | 100.0 | 18 | US-10-721-839-12 | Sequence 12, Appl |
| 16 | 66 | 100.0 | 29 | US-10-060-102-8 | Sequence 8, Appl |
| 17 | 66 | 100.0 | 29 | US-10-721-839-8 | Sequence 8, Appl |
| 18 | 64 | 97.0 | 14 | US-10-060-102-19 | Sequence 19, Appl |
| 19 | 64 | 97.0 | 14 | US-10-060-102-19 | Sequence 19, Appl |
| 20 | 64 | 97.0 | 14 | US-10-060-102-20 | Sequence 20, Appl |
| 21 | 64 | 97.0 | 14 | US-10-721-839-19 | Sequence 19, Appl |
| 22 | 64 | 97.0 | 16 | US-10-721-839-20 | Sequence 20, Appl |
| 23 | 64 | 97.0 | 16 | US-10-060-102-15 | Sequence 15, Appl |
| 24 | 64 | 97.0 | 16 | US-10-721-839-15 | Sequence 15, Appl |
| 25 | 64 | 97.0 | 18 | US-10-060-102-10 | Sequence 10, Appl |
| 26 | 64 | 97.0 | 18 | US-10-060-102-11 | Sequence 11, Appl |
| 27 | 64 | 97.0 | 18 | US-10-721-839-10 | Sequence 10, Appl |
| 28 | 61 | 92.4 | 18 | US-09-840-009-4 | Sequence 4, Appl |
| 29 | 61 | 92.4 | 18 | US-09-840-009-8 | Sequence 8, Appl |
| 30 | 61 | 92.4 | 18 | US-09-840-009-11 | Sequence 11, Appl |
| 31 | 61 | 92.4 | 18 | US-09-840-009-15 | Sequence 15, Appl |
| 32 | 61 | 92.4 | 18 | US-09-840-009-18 | Sequence 18, Appl |
| 33 | 61 | 92.4 | 18 | US-09-840-009-22 | Sequence 22, Appl |
| 34 | 61 | 92.4 | 18 | US-09-840-009-25 | Sequence 25, Appl |
| 35 | 61 | 92.4 | 18 | US-09-840-009-29 | Sequence 29, Appl |
| 36 | 61 | 92.4 | 18 | US-10-060-102-25 | Sequence 25, Appl |
| 37 | 61 | 92.4 | 18 | US-10-721-839-25 | Sequence 25, Appl |
| 38 | 60 | 90.9 | 18 | US-09-840-009-5 | Sequence 5, Appl |
| 39 | 60 | 90.9 | 18 | US-09-840-009-12 | Sequence 12, Appl |
| 40 | 60 | 90.9 | 18 | US-09-840-009-19 | Sequence 19, Appl |
| 41 | 60 | 90.9 | 18 | US-09-840-009-26 | Sequence 26, Appl |
| 42 | 59 | 89.4 | 18 | US-09-840-009-6 | Sequence 6, Appl |
| 43 | 59 | 89.4 | 18 | US-09-840-009-7 | Sequence 7, Appl |
| 44 | 59 | 89.4 | 18 | US-09-840-009-13 | Sequence 13, Appl |
| 45 | 59 | 89.4 | 18 | US-09-840-009-14 | Sequence 14, Appl |

ALIGNMENTS

RESULT 1
US-10-060-102-13
Sequence 13, Application US/10060102
Publication No. US2003002829A1
GENERAL INFORMATION:
APPLICANT: MAURY, WENDY
APPLICANT: STAPLETON, JACK
APPLICANT: ROLLER, RICHARD
APPLICANT: STINSKI, MARK
APPLICANT: MCCRAY, PAUL B.
APPLICANT: TACK, BRIAN
TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMAL
FILE REFERENCE: IOWA:035US
CURRENT APPLICATION NUMBER: US/10/060,102
CURRENT FILING DATE: 2002-02-22
PRIOR APPLICATION NUMBER: 60/309,368
PRIOR FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/265,270
PRIOR FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-060-102-13

Query Match 100.0%; Score 66; DB 14; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00056;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LRRIRKIIHIYK 14

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:18:40 ; Search time 13.2961 Seconds

(without alignments)
78.601 Million cell updates/sec

Title: US-09-642-744D-12

Sequence: 1 LRRIRKIHIIKK 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
- 2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
- 3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
- 4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
- 5: /cgn2_6/ptodata/1/1aa/6C.COMB.pep.*
- 6: /cgn2_6/ptodata/1/1aa/6D.COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the change being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|------------------|
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| 2 | 66 | 100.0 | 18 | 4 | US-09-840-009-9 |
| 3 | 66 | 100.0 | 18 | 4 | US-09-840-009-16 |
| 4 | 66 | 100.0 | 18 | 4 | US-09-840-009-23 |
| 5 | 66 | 100.0 | 18 | 4 | US-09-840-009-30 |
| 6 | 61 | 92.4 | 18 | 4 | US-09-840-009-4 |
| 7 | 61 | 92.4 | 18 | 4 | US-09-840-009-8 |
| 8 | 61 | 92.4 | 18 | 4 | US-09-840-009-11 |
| 9 | 61 | 92.4 | 18 | 4 | US-09-840-009-15 |
| 10 | 61 | 92.4 | 18 | 4 | US-09-840-009-18 |
| 11 | 61 | 92.4 | 18 | 4 | US-09-840-009-22 |
| 12 | 61 | 92.4 | 18 | 4 | US-09-840-009-25 |
| 13 | 61 | 92.4 | 18 | 4 | US-09-840-009-29 |
| 14 | 60 | 90.9 | 18 | 4 | US-09-840-009-12 |
| 15 | 60 | 90.9 | 18 | 4 | US-09-840-009-19 |
| 16 | 60 | 90.9 | 18 | 4 | US-09-840-009-26 |
| 17 | 60 | 90.9 | 18 | 4 | US-09-840-009-33 |
| 18 | 59 | 89.4 | 18 | 4 | US-09-840-009-6 |
| 19 | 59 | 89.4 | 18 | 4 | US-09-840-009-7 |
| 20 | 59 | 89.4 | 18 | 4 | US-09-840-009-13 |
| 21 | 59 | 89.4 | 18 | 4 | US-09-840-009-14 |
| 22 | 59 | 89.4 | 18 | 4 | US-09-840-009-20 |
| 23 | 59 | 89.4 | 18 | 4 | US-09-840-009-21 |
| 24 | 59 | 89.4 | 18 | 4 | US-09-840-009-27 |
| 25 | 59 | 89.4 | 18 | 4 | US-09-840-009-28 |
| 26 | 58 | 87.9 | 18 | 4 | US-09-840-009-3 |
| 27 | 58 | 87.9 | 18 | 4 | US-09-840-009-10 |

| | | | | | | |
|----|----|------|-----|---|---------------------|-------------------|
| 28 | 58 | 87.9 | 18 | 4 | US-09-840-009-17 | Sequence 17, Appl |
| 29 | 58 | 87.9 | 18 | 4 | US-09-840-009-24 | Sequence 24, Appl |
| 30 | 58 | 87.9 | 18 | 4 | US-09-840-009-31 | Sequence 31, Appl |
| 31 | 58 | 87.9 | 18 | 4 | US-09-840-009-34 | Sequence 34, Appl |
| 32 | 58 | 87.9 | 18 | 4 | US-09-840-009-35 | Sequence 35, Appl |
| 33 | 50 | 75.8 | 18 | 4 | US-09-840-009-32 | Sequence 32, Appl |
| 34 | 50 | 75.8 | 18 | 4 | US-09-840-009-33 | Sequence 33, Appl |
| 35 | 50 | 75.8 | 18 | 4 | US-09-840-009-36 | Sequence 36, Appl |
| 36 | 50 | 75.8 | 18 | 4 | US-09-840-009-37 | Sequence 37, Appl |
| 37 | 46 | 69.7 | 18 | 4 | US-09-840-009-1 | Sequence 1, Appl |
| 38 | 42 | 63.6 | 160 | 4 | US-09-917-340-36 | Sequence 36, Appl |
| 39 | 41 | 62.1 | 337 | 4 | US-09-538-092-38 | Sequence 38, Appl |
| 40 | 40 | 60.6 | 24 | 4 | US-09-785-059B-5 | Sequence 5, Appl |
| 41 | 40 | 60.6 | 36 | 4 | US-09-785-059B-6 | Sequence 6, Appl |
| 42 | 40 | 60.6 | 42 | 4 | US-09-785-059B-7 | Sequence 7, Appl |
| 43 | 40 | 60.6 | 48 | 4 | US-09-785-059B-8 | Sequence 8, Appl |
| 44 | 39 | 59.1 | 391 | 3 | US-09-134-001C-5234 | Sequence 5234, Ap |
| 45 | 38 | 57.6 | 149 | 4 | US-09-774-639-304 | Sequence 304, App |

ALIGNMENTS

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RESULT 1
US-09-840-009-2
; Sequence 2, Application US/09840009
; Patent No. 6492328
; GENERAL INFORMATION:
; APPLICANT: Lehner, Robert I.
; APPLICANT: Marling, Alan J.
; APPLICANT: Tack, Brian F.
; TITLE OF INVENTION: NOVISPINS: ANTIMICROBIAL PEPTIDES
; FILE REFERENCE: 06510-195W0
; CURRENT APPLICATION NUMBER: US/09/840, 009
; PRIOR FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 09/606, 858
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic antimicrobial peptide
US-09-840-009-2

Query Match          100.0%   Score 66;   DB 4;   Length 18;
Best Local Similarity 100.0%   Pred. No. 0.00036;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LRRIRKIHIIKK 14
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Db      3 LRRIRKIHIIKK 16

RESULT 2
US-09-840-009-9
; Sequence 9, Application US/09840009
; Patent No. 6492328
; GENERAL INFORMATION:
; APPLICANT: Lehner, Robert I.
; APPLICANT: Marling, Alan J.
; APPLICANT: Tack, Brian F.
; TITLE OF INVENTION: NOVISPINS: ANTIMICROBIAL PEPTIDES
; FILE REFERENCE: 06510-195W0
; CURRENT APPLICATION NUMBER: US/09/840, 009
; PRIOR FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 09/606, 858
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 9
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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:17:55 ; Search time 49.0782 Seconds
(without alignments)
110.327 Million cell updates/sec

Title: US-09-642-744D-12

Sequence: 1 LRRIRKIHIIKK 14

Scoring table: BLOSUM62

Gap 10.0, Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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3: geneeqp20008:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | ID | Description |
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| 1 | 66 | 100.0 | 14 | AA70658 Ovine SMA |
| 2 | 66 | 100.0 | 14 | AA70659 Ovine SMA |
| 3 | 66 | 100.0 | 14 | ABP53280 Synthetic |
| 4 | 66 | 100.0 | 14 | ABP53285 Synthetic |
| 5 | 66 | 100.0 | 16 | AA70656 Ovine SMA |
| 6 | 66 | 100.0 | 16 | ABP53281 Synthetic |
| 7 | 66 | 100.0 | 18 | AA70655 Ovine SMA |
| 8 | 66 | 100.0 | 18 | AA70648 Ovine SMA |
| 9 | 66 | 100.0 | 18 | AA70682 D11-nov1 |
| 10 | 66 | 100.0 | 18 | AA70685 D11-nov1 |
| 11 | 66 | 100.0 | 18 | AA70684 D11-nov1 |
| 12 | 66 | 100.0 | 18 | AA70685 D11-nov1 |
| 13 | 66 | 100.0 | 18 | AA70685 D11-nov1 |
| 14 | 66 | 100.0 | 18 | AA70685 D11-nov1 |
| 15 | 66 | 100.0 | 18 | AA70685 D11-nov1 |
| 16 | 66 | 100.0 | 18 | AA70685 D11-nov1 |
| 17 | 66 | 100.0 | 18 | AA70685 D11-nov1 |
| 18 | 66 | 100.0 | 18 | AA70685 D11-nov1 |
| 19 | 66 | 100.0 | 18 | AA70685 D11-nov1 |
| 20 | 66 | 100.0 | 18 | AA70685 D11-nov1 |
| 21 | 66 | 100.0 | 18 | AA70685 D11-nov1 |
| 22 | 66 | 100.0 | 18 | AA70685 D11-nov1 |
| 23 | 66 | 100.0 | 18 | AA70685 D11-nov1 |
| 24 | 66 | 100.0 | 18 | AA70685 D11-nov1 |
| 25 | 66 | 100.0 | 18 | AA70685 D11-nov1 |

| | | | | |
|----|----|------|----|--------------------|
| 26 | 64 | 97.0 | 18 | ABP53277 Synthetic |
| 27 | 64 | 97.0 | 20 | AA70653 Ovine SMA |
| 28 | 62 | 93.9 | 13 | AA70663 Ovine SMA |
| 29 | 61 | 92.4 | 13 | AA70662 Ovine SMA |
| 30 | 61 | 92.4 | 18 | AA70662 Ovine SMA |
| 31 | 61 | 92.4 | 18 | AA70662 Ovine SMA |
| 32 | 61 | 92.4 | 18 | AA70662 Ovine SMA |
| 33 | 61 | 92.4 | 18 | AA70662 Ovine SMA |
| 34 | 61 | 92.4 | 18 | AA70662 Ovine SMA |
| 35 | 61 | 92.4 | 18 | AA70662 Ovine SMA |
| 36 | 61 | 92.4 | 18 | AA70662 Ovine SMA |
| 37 | 61 | 92.4 | 18 | AA70662 Ovine SMA |
| 38 | 61 | 92.4 | 18 | AA70662 Ovine SMA |
| 39 | 60 | 90.9 | 18 | AA70662 Ovine SMA |
| 40 | 60 | 90.9 | 18 | AA70662 Ovine SMA |
| 41 | 60 | 90.9 | 18 | AA70662 Ovine SMA |
| 42 | 60 | 90.9 | 18 | AA70662 Ovine SMA |
| 43 | 59 | 89.4 | 18 | AA70662 Ovine SMA |
| 44 | 59 | 89.4 | 18 | AA70662 Ovine SMA |
| 45 | 59 | 89.4 | 18 | AA70662 Ovine SMA |

ALIGNMENTS

| | |
|----------|--|
| RESULT 1 | AA70658 strand; peptide, 14 AA. |
| ID | AA70658 |
| XX | AA70658 |
| AC | AA70658 |
| XX | AA70658 |
| DT | 15-MAY-2001 (first entry) |
| XX | 15-MAY-2001 (first entry) |
| DE | Ovine SMA 29 cathelicidin derived antimicrobial peptide SEQ ID NO.11. |
| XX | Ovine SMA 29 cathelicidin derived antimicrobial peptide SEQ ID NO.11. |
| KW | Ovine, SMAP29, lupine, RCAP 18, cathelicidin, antimicrobial, bactericidal, antibiotic, antiviral, microbial growth inhibitor, proliferation inhibitor, gene therapy, Pseudomonas aeruginosa, Burkholderia cepacia, Alcaligenes, Xanthomonas. |
| KM | Ovine, SMAP29, lupine, RCAP 18, cathelicidin, antimicrobial, bactericidal, antibiotic, antiviral, microbial growth inhibitor, proliferation inhibitor, gene therapy, Pseudomonas aeruginosa, Burkholderia cepacia, Alcaligenes, Xanthomonas. |
| OS | Ovis aries. |
| XX | Ovis aries. |
| PN | WO200112668-A1. |
| XX | WO200112668-A1. |
| PD | 22-FEB-2001. |
| XX | 22-FEB-2001. |
| PE | 18-AUG-2000; 2000MO-US022781. |
| XX | 18-AUG-2000; 2000MO-US022781. |
| PR | 18-AUG-1999; 99US-0149886P. |
| XX | 18-AUG-1999; 99US-0149886P. |
| PA | (IOWA) UNIV IOWA RES FOUND. |
| XX | (IOWA) UNIV IOWA RES FOUND. |
| PI | (REGC) UNIV CALIFORNIA. |
| XX | (REGC) UNIV CALIFORNIA. |
| DR | Tack BE, Mccrery P, Welsh M, Travis SM, Lehrer R; WPI; 2001-234911/24. |
| XX | Tack BE, Mccrery P, Welsh M, Travis SM, Lehrer R; WPI; 2001-234911/24. |
| PT | New antimicrobial peptides useful as antibiotics for inhibiting growth and proliferation of microbes, and for treating microbial infections. |
| XX | New antimicrobial peptides useful as antibiotics for inhibiting growth and proliferation of microbes, and for treating microbial infections. |
| PS | Claim 1, Page 103; 137pp; English. |
| XX | Claim 1, Page 103; 137pp; English. |
| CC | AA70648 to AA70675 represent antimicrobial peptides (I), of which AA70648 to AA70664, AA70667 and AA70675 are derived from the ovine SMAP 29 cathelicidin family peptide, and AA70665 to AA70673 are derived from the lupine RCAP 18 cathelicidin family peptide. (I) have antibiotic, antitumor and antiviral activities, and can be used as microbial growth and proliferation inhibitors and in gene therapy. (II) are useful for inhibiting microbial growth in an environment capable of sustaining such growth, for inhibiting microbial growth or strain in a host, and inhibiting the growth of drug-resistant microbial strains such as Pseudomonas aeruginosa, Burkholderia cepacia, Alcaligenes and Xanthomonas |
| XX | AA70648 to AA70675 represent antimicrobial peptides (I), of which AA70648 to AA70664, AA70667 and AA70675 are derived from the ovine SMAP 29 cathelicidin family peptide, and AA70665 to AA70673 are derived from the lupine RCAP 18 cathelicidin family peptide. (I) have antibiotic, antitumor and antiviral activities, and can be used as microbial growth and proliferation inhibitors and in gene therapy. (II) are useful for inhibiting microbial growth in an environment capable of sustaining such growth, for inhibiting microbial growth or strain in a host, and inhibiting the growth of drug-resistant microbial strains such as Pseudomonas aeruginosa, Burkholderia cepacia, Alcaligenes and Xanthomonas |

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: May 2, 2005, 12:17:06 ; Search time 43.6816 Seconds
(without alignments)
164.122 Million cell updates/sec

Title: US-09-642-744D-11
Perfect score: 66
Sequence: 1 LRRIRKIHIIKK 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 43 | 65.2 | 638 | 2 | Q8D796 |
| 2 | 43 | 65.2 | 660 | 2 | Q7MEAO |
| 3 | 42 | 63.6 | 125 | 2 | Q9AVZ1 |
| 4 | 42 | 63.6 | 160 | 1 | SCS1_SHEEP |
| 5 | 42 | 63.6 | 160 | 1 | SCS2_SHEEP |
| 6 | 42 | 63.6 | 308 | 2 | Q8RC7 |
| 7 | 42 | 63.6 | 500 | 1 | TF3B_SCHPO |
| 8 | 41 | 62.1 | 41 | 2 | Q48971 |
| 9 | 41 | 62.1 | 217 | 2 | Q977R2 |
| 10 | 41 | 62.1 | 337 | 1 | YBZ1_YEAST |
| 11 | 41 | 62.1 | 414 | 2 | Q947U2 |
| 12 | 41 | 62.1 | 414 | 2 | Q7XEX8 |
| 13 | 41 | 62.1 | 613 | 1 | DEAD_HAEIN |
| 14 | 41 | 62.1 | 670 | 1 | REP_BUCBP |
| 15 | 40 | 60.6 | 256 | 2 | Q83CP2 |
| 16 | 40 | 60.6 | 370 | 2 | Q67743 |
| 17 | 40 | 60.6 | 452 | 2 | Q7N787 |
| 18 | 40 | 60.6 | 461 | 2 | Q8TBM2 |
| 19 | 40 | 60.6 | 475 | 2 | Q7SGI8 |
| 20 | 40 | 60.6 | 867 | 2 | Q28391 |
| 21 | 39 | 59.1 | 202 | 1 | HAM1_AQUAE |
| 22 | 39 | 59.1 | 220 | 2 | Q92CL5 |
| 23 | 39 | 59.1 | 250 | 2 | Q7W5P0 |
| 24 | 39 | 59.1 | 250 | 2 | Q7WCY5 |
| 25 | 39 | 59.1 | 258 | 2 | Q8M771 |
| 26 | 39 | 59.1 | 349 | 2 | Q736D5 |
| 27 | 39 | 59.1 | 349 | 2 | Q81P89 |
| 28 | 39 | 59.1 | 349 | 2 | Q6HHI2 |
| 29 | 39 | 59.1 | 407 | 2 | Q9UTH1 |
| 30 | 39 | 59.1 | 428 | 2 | Q8TXS5 |
| 31 | 39 | 59.1 | 483 | 2 | Q9KR81 |

| | | | | | | |
|----|----|------|------|---|------------|------------------------|
| 32 | 39 | 59.1 | 598 | 2 | Q7VTH0 | Q7VTH0 bordetella |
| 33 | 39 | 59.1 | 838 | 2 | Q9DVL4 | Q9DVL4 human immun |
| 34 | 39 | 59.1 | 903 | 2 | Q9SWA7 | Q9SWA7 bulla goud |
| 35 | 39 | 59.1 | 967 | 2 | Q7R084 | Q7R084 plasmodium |
| 36 | 39 | 59.1 | 1157 | 2 | Q7R0N5 | Q7R0N5 plasmodium |
| 37 | 39 | 59.1 | 1160 | 2 | Q7SBL3 | Q7SBL3 neurospora |
| 38 | 39 | 59.1 | 1226 | 2 | Q6LS73 | Q6LS73 oryza sativ |
| 39 | 39 | 59.1 | 1580 | 2 | Q7RMP4 | Q7RMP4 plasmodium |
| 40 | 39 | 59.1 | 2084 | 2 | Q8ILJ6 | Q8ILJ6 plasmodium |
| 41 | 39 | 59.1 | 4057 | 2 | Q8IUE7 | Q8IUE7 plasmodium |
| 42 | 38 | 57.6 | 87 | 1 | SSS1_SCYCA | SSS1_SCYCA scyllorhinu |
| 43 | 38 | 57.6 | 102 | 2 | Q8YXR8 | Q8YXR8 listeria mo |
| 44 | 38 | 57.6 | 102 | 2 | Q926Y2 | Q926Y2 listeria mo |
| 45 | 38 | 57.6 | 102 | 2 | Q71VZ6 | Q71VZ6 listeria mo |

ALIGNMENTS

RESULT 1
Q8D796 PRELIMINARY; PRT; 638 AA.
ID Q8D796;
AC Q8D796;
DT 01-MAR-2003 (TREMblrel. 23, Created)
DT 01-MAR-2003 (TREMblrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
DE Predicted signal transduction protein.
GN OrderedLocusNames=V20264;
OS Vibrio vulnificus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrrio.
OX NCBI_TaxID=672;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CMP6;
RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
RA Choy H.E.;
RT "Complete genome sequence of Vibrio vulnificus CMP6."
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL, AE016808; AA007230.1; --
DR InterPro; IPR001633; EAL.
DR InterPro; IPR003018; GAF.
DR InterPro; IPR000160; GDEF.
DR Pfam; PF00563; EAL; 1.
DR Pfam; PF00590; GAF; 1.
DR Pfam; PF00990; GDEF; 1.
DR SMART; SM00052; DUF2; 1.
DR SMART; SM00065; GAF; 1.
DR TIGRFAMs; TIGR00254; GDEF; 1.
DR PROSITE; PS50883; EAL; 1.
DR PROSITE; PS50887; GDEF; 1.
KW Complete proteome.
SQ SEQUENCE 638 AA; 72187 MW; 7D13E28DF3A3F099 CRC64;
Query Match 65.2%; Score 43; DB 2; Length 638;
Best Local Similarity 61.5%; Pred. No. 65;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 2 RRIIRKIHIIKK 14
DB 566 KEIRSIHVAKK 578
RESULT 2
ID Q7MEAO PRELIMINARY; PRT; 660 AA.
AC Q7MEAO;
DT 01-MAR-2004 (TREMblrel. 26, Created)
DT 01-MAR-2004 (TREMblrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
DE GDBF family protein.
GN OrderedLocusNames=VVA0770;
OS Vibrio vulnificus (strain VJ016).

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 2, 2005, 13:03:56 ; Search time 38.0894 Seconds

(without alignments)
122.435 Million cell updates/sec

Title: US-09-642-744d-11

Perfect score: 66

Sequence: 1 LRRIRKIHIIKK 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1426032 seqs, 33106140 residues

Total number of hits satisfying chosen parameters: 1426032

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCR_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/PCRUS_PUBCOMB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

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14: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*

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19: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*

20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 66 | 100.0 | 14 | US-10-060-102-13 | Sequence 13, Appl |
| 2 | 66 | 100.0 | 14 | US-10-060-102-18 | Sequence 18, Appl |
| 3 | 66 | 100.0 | 14 | US-10-721-839-13 | Sequence 13, Appl |
| 4 | 66 | 100.0 | 14 | US-10-721-839-13 | Sequence 13, Appl |
| 5 | 66 | 100.0 | 14 | US-10-721-839-13 | Sequence 13, Appl |
| 6 | 66 | 100.0 | 14 | US-10-721-839-13 | Sequence 13, Appl |
| 7 | 66 | 100.0 | 14 | US-10-721-839-13 | Sequence 13, Appl |
| 8 | 66 | 100.0 | 14 | US-10-721-839-13 | Sequence 13, Appl |
| 9 | 66 | 100.0 | 14 | US-10-721-839-13 | Sequence 13, Appl |
| 10 | 66 | 100.0 | 14 | US-10-721-839-13 | Sequence 13, Appl |
| 11 | 66 | 100.0 | 14 | US-10-721-839-13 | Sequence 13, Appl |
| 12 | 66 | 100.0 | 14 | US-10-721-839-13 | Sequence 13, Appl |
| 13 | 66 | 100.0 | 14 | US-10-721-839-13 | Sequence 13, Appl |

| | | | | | |
|----|----|-------|----|------------------|-------------------|
| 14 | 66 | 100.0 | 18 | US-10-721-839-9 | Sequence 9, Appl |
| 15 | 66 | 100.0 | 18 | US-10-721-839-12 | Sequence 12, Appl |
| 16 | 66 | 100.0 | 29 | US-10-060-102-8 | Sequence 8, Appl |
| 17 | 66 | 100.0 | 29 | US-10-060-102-8 | Sequence 8, Appl |
| 18 | 66 | 100.0 | 14 | US-10-060-102-19 | Sequence 19, Appl |
| 19 | 66 | 100.0 | 14 | US-10-060-102-19 | Sequence 19, Appl |
| 20 | 66 | 100.0 | 14 | US-10-060-102-20 | Sequence 20, Appl |
| 21 | 66 | 100.0 | 14 | US-10-060-102-20 | Sequence 20, Appl |
| 22 | 66 | 100.0 | 14 | US-10-060-102-20 | Sequence 20, Appl |
| 23 | 66 | 100.0 | 14 | US-10-060-102-20 | Sequence 20, Appl |
| 24 | 66 | 100.0 | 14 | US-10-060-102-20 | Sequence 20, Appl |
| 25 | 66 | 100.0 | 14 | US-10-060-102-20 | Sequence 20, Appl |
| 26 | 66 | 100.0 | 14 | US-10-060-102-20 | Sequence 20, Appl |
| 27 | 66 | 100.0 | 14 | US-10-060-102-20 | Sequence 20, Appl |
| 28 | 66 | 100.0 | 14 | US-10-060-102-20 | Sequence 20, Appl |
| 29 | 66 | 100.0 | 14 | US-10-060-102-20 | Sequence 20, Appl |
| 30 | 66 | 100.0 | 14 | US-10-060-102-20 | Sequence 20, Appl |
| 31 | 66 | 100.0 | 14 | US-10-060-102-20 | Sequence 20, Appl |
| 32 | 66 | 100.0 | 14 | US-10-060-102-20 | Sequence 20, Appl |
| 33 | 66 | 100.0 | 14 | US-10-060-102-20 | Sequence 20, Appl |
| 34 | 66 | 100.0 | 14 | US-10-060-102-20 | Sequence 20, Appl |
| 35 | 66 | 100.0 | 14 | US-10-060-102-20 | Sequence 20, Appl |
| 36 | 66 | 100.0 | 14 | US-10-060-102-20 | Sequence 20, Appl |
| 37 | 66 | 100.0 | 14 | US-10-060-102-20 | Sequence 20, Appl |
| 38 | 66 | 100.0 | 14 | US-10-060-102-20 | Sequence 20, Appl |
| 39 | 66 | 100.0 | 14 | US-10-060-102-20 | Sequence 20, Appl |
| 40 | 66 | 100.0 | 14 | US-10-060-102-20 | Sequence 20, Appl |
| 41 | 66 | 100.0 | 14 | US-10-060-102-20 | Sequence 20, Appl |
| 42 | 66 | 100.0 | 14 | US-10-060-102-20 | Sequence 20, Appl |
| 43 | 66 | 100.0 | 14 | US-10-060-102-20 | Sequence 20, Appl |
| 44 | 66 | 100.0 | 14 | US-10-060-102-20 | Sequence 20, Appl |
| 45 | 66 | 100.0 | 14 | US-10-060-102-20 | Sequence 20, Appl |

ALIGNMENTS

RESULT 1

US-10-060-102-13

Sequence 13, Application US/10060102

Publication No. US20030022829A1

GENERAL INFORMATION:

APPLICANT: MAURY, WENDY

APPLICANT: STABLETON, JACK

APPLICANT: ROLLER, RICHARD

APPLICANT: STINSKI, MARK

APPLICANT: MCCRAY, PAUL B.

APPLICANT: TACK, BRIAN

TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIVATE THETA DEFENSINS AND MAMMAL

FILE REFERENCE: IOWA.035US

CURRENT APPLICATION NUMBER: US/10/060,102

PRIOR FILING DATE: 2002-02-22

PRIOR APPLICATION NUMBER: 60/309,368

PRIOR FILING DATE: 2001-08-01

NUMBER OF SEQ ID NOS: 32

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 13

LENGTH: 14

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-10-060-102-13

Query Match

Best Local Similarity 100.0%; Score 66; DB 14; Length 14;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LRRIRKIHIIKK 14

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:18:40 ; Search time 13.2961 Seconds

(without alignments)
78.601 Million cell updates/sec

Title: US-09-642-744D-11

Perfect score: 66

Sequence: 1 LRRIRKIHIIKK 14

Scoring table: BIOSUM62

Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: Issued Patents AA:*

- 1: /cgn2_6/prodata/1/1aa/5A COMB.pep.*
- 2: /cgn2_6/prodata/1/1aa/5B COMB.pep.*
- 3: /cgn2_6/prodata/1/1aa/6A COMB.pep.*
- 4: /cgn2_6/prodata/1/1aa/6B COMB.pep.*
- 5: /cgn2_6/prodata/1/1aa/6C COMB.pep.*
- 6: /cgn2_6/prodata/1/1aa/6D COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|------------------|
| 1 | 66 | 100.0 | 18 | 4 | US-09-840-009-2 |
| 2 | 66 | 100.0 | 18 | 4 | US-09-840-009-9 |
| 3 | 66 | 100.0 | 18 | 4 | US-09-840-009-16 |
| 4 | 66 | 100.0 | 18 | 4 | US-09-840-009-23 |
| 5 | 66 | 100.0 | 18 | 4 | US-09-840-009-30 |
| 6 | 61 | 92.4 | 18 | 4 | US-09-840-009-4 |
| 7 | 61 | 92.4 | 18 | 4 | US-09-840-009-8 |
| 8 | 61 | 92.4 | 18 | 4 | US-09-840-009-11 |
| 9 | 61 | 92.4 | 18 | 4 | US-09-840-009-15 |
| 10 | 61 | 92.4 | 18 | 4 | US-09-840-009-18 |
| 11 | 61 | 92.4 | 18 | 4 | US-09-840-009-22 |
| 12 | 61 | 92.4 | 18 | 4 | US-09-840-009-25 |
| 13 | 61 | 92.4 | 18 | 4 | US-09-840-009-29 |
| 14 | 60 | 90.9 | 18 | 4 | US-09-840-009-5 |
| 15 | 60 | 90.9 | 18 | 4 | US-09-840-009-12 |
| 16 | 60 | 90.9 | 18 | 4 | US-09-840-009-19 |
| 17 | 60 | 90.9 | 18 | 4 | US-09-840-009-26 |
| 18 | 59 | 89.4 | 18 | 4 | US-09-840-009-7 |
| 19 | 59 | 89.4 | 18 | 4 | US-09-840-009-13 |
| 20 | 59 | 89.4 | 18 | 4 | US-09-840-009-14 |
| 21 | 59 | 89.4 | 18 | 4 | US-09-840-009-20 |
| 22 | 59 | 89.4 | 18 | 4 | US-09-840-009-21 |
| 23 | 59 | 89.4 | 18 | 4 | US-09-840-009-27 |
| 24 | 59 | 89.4 | 18 | 4 | US-09-840-009-28 |
| 25 | 59 | 89.4 | 18 | 4 | US-09-840-009-3 |
| 26 | 58 | 87.9 | 18 | 4 | US-09-840-009-10 |
| 27 | 58 | 87.9 | 18 | 4 | US-09-840-009-10 |

| | | | | | | |
|----|----|------|-----|---|---------------------|-------------------|
| 28 | 58 | 87.9 | 18 | 4 | US-09-840-009-17 | Sequence 17, Appl |
| 29 | 58 | 87.9 | 18 | 4 | US-09-840-009-24 | Sequence 24, Appl |
| 30 | 58 | 87.9 | 18 | 4 | US-09-840-009-31 | Sequence 31, Appl |
| 31 | 58 | 87.9 | 18 | 4 | US-09-840-009-35 | Sequence 35, Appl |
| 32 | 58 | 87.9 | 18 | 4 | US-09-840-009-35 | Sequence 32, Appl |
| 33 | 50 | 75.8 | 18 | 4 | US-09-840-009-32 | Sequence 33, Appl |
| 34 | 50 | 75.8 | 18 | 4 | US-09-840-009-36 | Sequence 36, Appl |
| 35 | 50 | 75.8 | 18 | 4 | US-09-840-009-36 | Sequence 37, Appl |
| 36 | 50 | 75.8 | 18 | 4 | US-09-840-009-37 | Sequence 38, Appl |
| 37 | 46 | 69.7 | 18 | 4 | US-09-840-009-37 | Sequence 39, Appl |
| 38 | 42 | 63.6 | 160 | 4 | US-09-917-340-36 | Sequence 40, Appl |
| 39 | 41 | 62.1 | 337 | 4 | US-09-538-092-38 | Sequence 41, Appl |
| 40 | 40 | 60.6 | 24 | 4 | US-09-785-0598-5 | Sequence 42, Appl |
| 41 | 40 | 60.6 | 36 | 4 | US-09-785-0598-6 | Sequence 43, Appl |
| 42 | 40 | 60.6 | 42 | 4 | US-09-785-0598-7 | Sequence 44, Appl |
| 43 | 40 | 60.6 | 48 | 4 | US-09-785-0598-8 | Sequence 45, Appl |
| 44 | 39 | 59.1 | 391 | 3 | US-09-134-001C-5234 | Sequence 46, Appl |
| 45 | 38 | 57.6 | 149 | 4 | US-09-774-639-304 | Sequence 47, Appl |

ALIGNMENTS

RESULT 1
US-09-840-009-2
Sequence 2, Application US/09840009
Patent No. 6492328
GENERAL INFORMATION:
APPLICANT: Lehrer, Robert I.
APPLICANT: Tack, Brian F.
TITLE OF INVENTION: NOVIAPRINS: ANTIMICROBIAL PEPTIDES
FILE REFERENCE: 06510-195WO
CURRENT APPLICATION NUMBER: US/09/840,009
CURRENT FILING DATE: 2001-04-19
PRIOR APPLICATION NUMBER: US 09/606,858
PRIOR FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic antimicrobial peptide
US-09-840-009-2
Query Match 100.0%, Score 66, DB 4, Length 18,
Best Local Similarity 100.0%, Pred. No. 0.00036,
Matches 14, Conservative 0, Mismatches 0, Indels 0, Gaps 0;
QY 1 LRRIRKIHIIKK 14
DB 3 LRRIRKIHIIKK 16
RESULT 2
US-09-840-009-9
Sequence 9, Application US/09840009
Patent No. 6492328
GENERAL INFORMATION:
APPLICANT: Lehrer, Robert I.
APPLICANT: Tack, Brian F.
TITLE OF INVENTION: NOVIAPRINS: ANTIMICROBIAL PEPTIDES
FILE REFERENCE: 06510-195WO
CURRENT APPLICATION NUMBER: US/09/840,009
CURRENT FILING DATE: 2001-04-19
PRIOR APPLICATION NUMBER: US 09/606,858
PRIOR FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:17:55 ; Search time 49.0782 Seconds

(without alignments)
110.327 Million cell updates/sec

Title: US-09-642-744D-11
Sequence: 1 LRRIRKIHNIK 14

Scoring table: BLAST62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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2: geneseqp1990s:*
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4: geneseqp2001s:*
5: geneseqp2002s:*
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7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 2 | 66 | 100.0 | 14 | 4 AAB70659 | Aab70659 Ovine SMA |
| 3 | 66 | 100.0 | 14 | 5 ABP53280 | Abp53280 Synthetic |
| 4 | 66 | 100.0 | 14 | 5 ABP53285 | Abp53285 Synthetic |
| 5 | 66 | 100.0 | 16 | 4 AAB70656 | Aab70656 Ovine SMA |
| 6 | 66 | 100.0 | 16 | 5 ABP53281 | Abp53281 Synthetic |
| 7 | 66 | 100.0 | 18 | 4 AAB70655 | Aab70655 Ovine SMA |
| 8 | 66 | 100.0 | 18 | 4 AAB70648 | Aab70648 Ovine SMA |
| 9 | 66 | 100.0 | 18 | 5 AAE20882 | Aae20882 D11-novi |
| 10 | 66 | 100.0 | 18 | 5 AAE20885 | Aae20885 D11-novi |
| 11 | 66 | 100.0 | 18 | 5 AAE20854 | Aae20854 Ovisplrin |
| 12 | 66 | 100.0 | 18 | 5 AAE20861 | Aae20861 D16-nov18 |
| 13 | 66 | 100.0 | 18 | 5 AAE20868 | Aae20868 D17-nov18 |
| 14 | 66 | 100.0 | 18 | 5 ABP53276 | Abp53276 Synthetic |
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| 17 | 66 | 100.0 | 29 | 5 ABP53275 | Abp53275 Synthetic |
| 18 | 64 | 97.0 | 14 | 4 AAB70661 | Aab70661 Ovine SMA |
| 19 | 64 | 97.0 | 14 | 4 AAB70660 | Aab70660 Ovine SMA |
| 20 | 64 | 97.0 | 14 | 5 ABP53286 | Abp53286 Synthetic |
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| 22 | 64 | 97.0 | 16 | 4 AAB70657 | Aab70657 Ovine SMA |
| 23 | 64 | 97.0 | 16 | 5 ABP53282 | Abp53282 Synthetic |
| 24 | 64 | 97.0 | 18 | 4 AAB70654 | Aab70654 Ovine SMA |
| 25 | 64 | 97.0 | 18 | 5 ABP53278 | Abp53278 Synthetic |

| | | | | | |
|----|----|------|----|------------|--------------------|
| 26 | 64 | 97.0 | 18 | 5 ABP53277 | Abp53277 Synthetic |
| 27 | 64 | 97.0 | 20 | 4 AAB70653 | Aab70653 Ovine SMA |
| 28 | 62 | 93.9 | 13 | 4 AAB70663 | Aab70663 Ovine SMA |
| 29 | 61 | 92.4 | 13 | 4 AAB70662 | Aab70662 Ovine SMA |
| 30 | 61 | 92.4 | 18 | 5 AAE20870 | Aae20870 T10-nov18 |
| 31 | 61 | 92.4 | 18 | 5 AAE20860 | Aae20860 D16-nov18 |
| 32 | 61 | 92.4 | 18 | 5 AAE20881 | Aae20881 D11-nov18 |
| 33 | 61 | 92.4 | 18 | 5 AAE20867 | Aae20867 D17-nov18 |
| 34 | 61 | 92.4 | 18 | 5 AAE20874 | Aae20874 D10-nov18 |
| 35 | 61 | 92.4 | 18 | 5 AAE20863 | Aae20863 T7-nov18 |
| 36 | 61 | 92.4 | 18 | 5 AAE20877 | Aae20877 T11-nov18 |
| 37 | 61 | 92.4 | 18 | 5 AAE20856 | Aae20856 T6-nov18 |
| 38 | 60 | 90.9 | 18 | 5 ABP53292 | Abp53292 Synthetic |
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| 40 | 60 | 90.9 | 18 | 5 AAE20871 | Aae20871 S10-nov18 |
| 41 | 60 | 90.9 | 18 | 5 AAE20878 | Aae20878 S11-nov18 |
| 42 | 60 | 90.9 | 18 | 5 AAE20857 | Aae20857 S6-nov18 |
| 43 | 59 | 89.4 | 18 | 5 AAE20872 | Aae20872 E10-nov18 |
| 44 | 59 | 89.4 | 18 | 5 AAE20873 | Aae20873 D10-nov18 |
| 45 | 59 | 89.4 | 18 | 5 AAE20858 | Aae20858 E6-nov18 |

ALIGNMENTS

RESULT 1
AAB70658
ID AAB70658 standard; peptide; 14 AA.
XX
AC AAB70658;
XX
DT 15-MAY-2001 (first entry)
XX
DE Ovine SMAP 29 cathelicidin derived antimicrobial peptide SEQ ID NO:11.
XX
XX
KW Ovine; SMAP29; lupine; RCAP 18; cathelicidin; antimicrobial;
KW bactericidal; antibiotic; antiviral; microbial growth inhibitor;
KW proliferation inhibitor; gene therapy; Pseudomonas aeruginosa;
KW Burkholderia cepacia; Alcaligenes; Xanthomonas.
XX
OS Ovis aries.
XX
PN WO200112668-A1.
XX
PD 22-FEB-2001.
XX
PF 18-AUG-2000; 2000WO-US022781.
XX
PR 18-AUG-1999; 99US-0149886P.
XX
PA (IOWA) UNIV IOWA RES FOUND.
PA (REGC) UNIV CALIFORNIA.
XX
PI Tack BE, Mccray P, Welsh M, Travis SM, Lehrer R;
XX WPI; 2001-234911/24.
XX
PT New antimicrobial peptides useful as antibiotics for inhibiting growth
PT and proliferation of microbes, and for treating microbial infections.
XX
PS Claim 1; Page 103; 137pp; English.
XX
CC AAB70648 to AAB70675 represent antimicrobial peptides (I), of which
CC AAB70648 to AAB70664, AAB70674 and AAB70675 are derived from the ovine
CC SMAP 29 cathelicidin family peptide, and AAB70665 to AAB70673 are derived
CC from the lupine RCAP 18 cathelicidin family peptide. (I) have antibiotic,
CC antimicrobial and antiviral activities, and can be used as microbial
CC growth and proliferation inhibitors and in gene therapy. (I) are useful
CC for inhibiting microbial growth in an environment capable of sustaining
CC such growth, for inhibiting microbial growth or strain in a host, and
CC inhibiting the growth of drug-resistant microbial strains such as
CC Pseudomonas aeruginosa, Burkholderia cepacia, Alcaligenes and Xanthomonas
XX

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:17:06 ; Search time 49.9218 seconds

(without alignments)
164.122 Million cell updates/sec

Title: US-09-642-744d-10

Perfect score: 79

Sequence: 1 NRRIRKIIHIHKY 16

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*
1: uniProt_sprot.*
2: uniProt_trembl.*

SUMMARIES

| Result No. | Score | Query | Match | Length | DB | ID | Description |
|------------|-------|-------|-------|--------|------------|--------|--------------|
| 1 | 48 | 60.8 | 500 | 1 | TF3B_SCHPO | 09p610 | schizosacch |
| 2 | 47 | 59.5 | 160 | 1 | SCS1_SHEEP | P49928 | ovis aries |
| 3 | 47 | 59.5 | 160 | 1 | SCS2_SHEEP | P49929 | ovis aries |
| 4 | 45 | 57.0 | 182 | 2 | 0896E1 | 0896E1 | clostridium |
| 5 | 45 | 57.0 | 234 | 2 | 059264 | 059264 | clostridium |
| 6 | 45 | 57.0 | 308 | 2 | 08R2C7 | 08R2C7 | mus musculus |
| 7 | 45 | 57.0 | 834 | 2 | 07RRI0 | 07RRI0 | plasmidium |
| 8 | 44 | 55.7 | 231 | 2 | 08RAG4 | 08RAG4 | thermoanaer |
| 9 | 44 | 55.7 | 233 | 2 | 09L7X2 | 09L7X2 | clostridium |
| 10 | 44 | 55.7 | 233 | 2 | 08XJ18 | 08XJ18 | clostridium |
| 11 | 44 | 55.7 | 349 | 2 | 0736D5 | 0736D5 | bacillus ce |
| 12 | 44 | 55.7 | 349 | 2 | 081B89 | 081B89 | bacillus an |
| 13 | 44 | 55.7 | 349 | 2 | 06HHI2 | 06HHI2 | bacillus th |
| 14 | 44 | 55.7 | 402 | 2 | 081I43 | 081I43 | plasmidium |
| 15 | 44 | 55.7 | 420 | 1 | PR11_HUMAN | P49642 | homo sapien |
| 16 | 44 | 55.7 | 460 | 2 | 09VL03 | 09VL03 | drosofila |
| 17 | 44 | 55.7 | 549 | 2 | 081PC2 | 081PC2 | drosofila |
| 18 | 44 | 55.7 | 1137 | 2 | 06LFF7 | 06LFF7 | plasmidium |
| 19 | 44 | 55.7 | 1279 | 2 | 081B12 | 081B12 | plasmidium |
| 20 | 44 | 55.7 | 2084 | 2 | 081LW6 | 081LW6 | plasmidium |
| 21 | 44 | 55.7 | 6077 | 2 | 06LFF6 | 06LFF6 | plasmidium |
| 22 | 43 | 54.4 | 483 | 2 | P95941 | P95941 | bulfolobus |
| 23 | 43 | 54.4 | 638 | 2 | 08D796 | 08D796 | vibrio vuln |
| 24 | 43 | 54.4 | 660 | 2 | 07MEAO | 07MEAO | vibrio vuln |
| 25 | 43 | 54.4 | 867 | 2 | 028391 | 028391 | archaeoglob |
| 26 | 43 | 54.4 | 875 | 2 | 08R8R4 | 08R8R4 | thermoanaer |
| 27 | 43 | 54.4 | 878 | 2 | 07RY40 | 07RY40 | neurospora |
| 28 | 43 | 54.4 | 3267 | 2 | 081B20 | 081B20 | plasmidium |
| 29 | 42.5 | 53.8 | 301 | 2 | 07Q4C0 | 07Q4C0 | anopheles g |
| 30 | 42.5 | 53.8 | 314 | 2 | 065L76 | 065L76 | bacillus th |
| 31 | 42.5 | 53.8 | 324 | 2 | 062X75 | 062X75 | bacillus th |

| | | | | | | | |
|----|----|------|-----|---|------------|--------|--------------|
| 32 | 42 | 53.2 | 125 | 2 | 09AV21 | 09AV21 | guillardia |
| 33 | 42 | 53.2 | 146 | 1 | RUVX_MYCPU | 096013 | mycoplasma |
| 34 | 42 | 53.2 | 151 | 2 | 08R851 | 08R851 | thermoanaer |
| 35 | 42 | 53.2 | 157 | 2 | 07NA14 | 07NA14 | phototaxadu |
| 36 | 42 | 53.2 | 198 | 2 | 06LIE8 | 06LIE8 | picrophilus |
| 37 | 42 | 53.2 | 232 | 2 | 07MT01 | 07MT01 | porphyromon |
| 38 | 42 | 53.2 | 414 | 2 | 0947U2 | 0947U2 | oryza sativ |
| 39 | 42 | 53.2 | 414 | 2 | 07XEX8 | 07XEX8 | oryza sativ |
| 40 | 42 | 53.2 | 415 | 2 | 089045 | 089045 | rattus norv |
| 41 | 42 | 53.2 | 417 | 1 | PR11_MOUSE | P20664 | mus musculus |
| 42 | 42 | 53.2 | 530 | 2 | 09C2F6 | 09C2F6 | neurospora |
| 43 | 42 | 53.2 | 537 | 2 | 097WL6 | 097WL6 | sulfolobus |
| 44 | 42 | 53.2 | 678 | 2 | 07PBP0 | 07PBP0 | anopheles g |
| 45 | 42 | 53.2 | 684 | 2 | 07QNN1 | 07QNN1 | giardia lam |

ALIGNMENTS

RESULT 1
TF3B_SCHPO STANDARD, PRT, 500 AA.
AC 09p610, 09US04;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Transcription factor IIB 60 kDa subunit (TFIIB) (B-related factor)
DE (BRF) (TFIIB-related factor).
GN Name=brf1, ORFNames=SPBC13E7.10c, SPBC30D10.20;
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_Taxid:4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volskeert G., Aert R., Robben J., Grympez B.,
RA Welfens I., Vansirels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Medler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Leleau V., Motier S.,
RA Galibert M., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gallard C., Tallada V.A., Garzon A., Rhode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez J., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrett B.G., Nurse P.;
RL "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
[2]
INTERACTION WITH TBP.
RX MEDLINE=22569152; PubMed=12682361; DOI=10.1093/nar/gkq301;
RA Huang Y., McGillicuddy E., Weindl M., Dong S., Maraja R.J.;
RT "The fission yeast TFIIB-related factor limits RNA polymerase III to a
TBP-dependent pathway of TBP recruitment.";
RL Nucleic Acids Res. 31:2108-2116(2003).
CC -1- FUNCTION: General activator of RNA polymerase III transcription.
CC -1- COPACITOR: Binds 1 zinc ion per subunit (By similarity).

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:21:40 ; Search time 9.92179 Seconds
(without alignments)
155.160 Million cell updates/sec

Title: US-09-642-744D-10

Sequence: 1 NTRRIIRKIHIIRKY 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*

1: pir1:
2: pir2:
3: pir3:
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|----------------------------|
| 1 | 47 | 59.5 | 152 | 2 | S68411 cathelin-related p |
| 2 | 47 | 59.5 | 160 | 2 | S68412 cathelin-related p |
| 3 | 47 | 59.5 | 160 | 2 | S68228 myeloid antimicrob |
| 4 | 45 | 57.0 | 234 | 2 | D97108 DNA-dependent RNA |
| 5 | 45 | 57.0 | 234 | 2 | D97108 sick protein - C10 |
| 6 | 44 | 55.7 | 420 | 2 | S45630 DNA primase chain |
| 7 | 43 | 54.4 | 483 | 2 | S75369 DNA-directed RNA p |
| 8 | 43 | 54.4 | 867 | 2 | G69485 DNA-directed RNA p |
| 9 | 42 | 53.2 | 125 | 2 | A89114 hypothetical prote |
| 10 | 42 | 53.2 | 146 | 2 | D90581 conserved hypotet |
| 11 | 42 | 53.2 | 417 | 2 | A33269 DNA primase (EC 2. |
| 12 | 42 | 53.2 | 537 | 2 | C90389 conserved hypotet |
| 13 | 41 | 51.9 | 186 | 2 | B90116 hypothetical prote |
| 14 | 41 | 51.9 | 337 | 2 | S46010 hypothetical prote |
| 15 | 41 | 51.9 | 507 | 2 | T10753 intestinal DNA rep |
| 16 | 41 | 51.9 | 613 | 2 | F64056 probable ATP-depen |
| 17 | 40 | 50.6 | 105 | 2 | F71128 hypothetical prote |
| 18 | 40 | 50.6 | 177 | 2 | T28362 hypothetical prote |
| 19 | 40 | 50.6 | 221 | 2 | S39609 EBD2 protease - mal |
| 20 | 40 | 50.6 | 370 | 2 | C70464 GTP-binding protei |
| 21 | 40 | 50.6 | 791 | 2 | D82901 ATP-dependent prot |
| 22 | 40 | 50.6 | 1634 | 2 | E64410 DNA-directed RNA p |
| 23 | 40 | 50.6 | 1741 | 2 | T15978 hypothetical prote |
| 24 | 39.5 | 50.0 | 208 | 2 | G81196 N-(5'-phosphoribos |
| 25 | 39.5 | 50.0 | 208 | 2 | G81195 N-(5'-phosphoribos |
| 26 | 39.5 | 50.0 | 313 | 2 | A89971 probable phosphori |
| 27 | 39 | 49.4 | 41 | 2 | S77768 cmp-binding factor |
| 28 | 39 | 49.4 | 113 | 2 | G90223 hypothetical prote |
| 29 | 39 | 49.4 | 151 | 2 | H90035 DNA-directed RNA p |
| 30 | 39 | 49.4 | 151 | 2 | H90035 tear transcription |

| | | | | | |
|----|------|------|-----|---|---------------------------|
| 30 | 39 | 49.4 | 202 | 1 | H70318 conserved hypothet |
| 31 | 39 | 49.4 | 210 | 2 | AC1577 precortin isomeras |
| 32 | 39 | 49.4 | 292 | 2 | A97035 cation efflux syst |
| 33 | 39 | 49.4 | 319 | 1 | S19248 RNA-directed DNA p |
| 34 | 39 | 49.4 | 334 | 2 | B72301 endoglucanase - Th |
| 35 | 39 | 49.4 | 407 | 2 | T17888 hypothetical prote |
| 36 | 39 | 49.4 | 414 | 2 | G64091 cell division prot |
| 37 | 39 | 49.4 | 483 | 2 | B82160 hypothetical prote |
| 38 | 39 | 49.4 | 540 | 2 | T33982 hypothetical prote |
| 39 | 39 | 49.4 | 762 | 2 | S56141 HAKI protein - Yea |
| 40 | 38.5 | 48.7 | 381 | 1 | C6416 conserved hypothet |
| 41 | 38 | 48.1 | 87 | 2 | S00180 spermatid protein |
| 42 | 38 | 48.1 | 96 | 2 | C64354 hypothetical prote |
| 43 | 38 | 48.1 | 156 | 1 | D71689 hypothetical prote |
| 44 | 38 | 48.1 | 172 | 2 | T28288 ORF MSV127 hypothe |
| 45 | 38 | 48.1 | 189 | 2 | H96903 transcription regu |

ALIGNMENTS

RESULT 1

S68411

cathelin-related protein 2 precursor - sheep (fragment)

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000

C/Accession: S68411

R:Mahoney, M.M.; Lee, A.Y.; Brezinski-Caliguri, D.J.; Hutter, K.M.

FEBS Lett. 377, 519-522, 1995

A:Title: Molecular analysis of the sheep cathelin family reveals a novel antimicrobial

A:Reference number: S68411; MUID:96140581; PMID:8549789

A/Accession: S68411

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-152 <MAH>

A/Cross-references: EMBL:X92757

C:Genetics:

A:Gene: SC5-2

C:Superfamily: cathelin; cystatin homology

F:1-21/Domain: signal sequence #status predicted <SIG>

F:14-122/Domain: cystatin homology <CYS>

F:21-123/Domain: propeptide #status predicted <PRO>

F:124-152/Product: cathelin-related protein 2 #status predicted <MAT>

Query Match

Best Local Similarity 59.5%; Score 47; DB 2; Length 152;

Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 2 IRRIRKIHIIRKY 16

Db 126 IRRIRKIHIIRKY 140

RESULT 2

S68412

cathelin-related protein 1 precursor - sheep

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000

C/Accession: S68412

R:Mahoney, M.M.; Lee, A.Y.; Brezinski-Caliguri, D.J.; Hutter, K.M.

FEBS Lett. 377, 519-522, 1995

A:Title: Molecular analysis of the sheep cathelin family reveals a novel antimicrobial

A:Reference number: S68411; MUID:96140581; PMID:8549789

A/Accession: S68412

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-160 <MAH>

A/Cross-references: EMBL:X92758

C:Genetics:

A:Gene: SC5-1

C:Superfamily: cathelin; cystatin homology

F:1-29/Domain: signal sequence #status predicted <SIG>

F:22-130/Domain: cystatin homology <CYS>

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OM protein - protein search, using sw model

Run on: May 2, 2005, 13:03:56 ; Search time 43.5307 Seconds

(without alignments)
122.435 Million cell updates/sec

Title: US-09-642-744d-10

Sequence: 1 NRRIRKIHIIKKY 16

Scoring table:

BLOSUM62
Gap 10.0 , Gapext 0.5

Searched: 1426032 seqs, 33106140 residues

Total number of hits satisfying chosen parameters: 1426032

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|------------------|
| 1 | 79 | 100.0 | 16 | 14 | US-10-060-102-15 |
| 2 | 79 | 100.0 | 16 | 15 | US-10-721-839-15 |
| 3 | 79 | 100.0 | 16 | 15 | US-10-060-102-10 |
| 4 | 79 | 100.0 | 16 | 14 | US-10-060-102-11 |
| 5 | 79 | 100.0 | 16 | 15 | US-10-721-839-10 |
| 6 | 79 | 100.0 | 16 | 15 | US-10-721-839-11 |
| 7 | 77 | 97.5 | 16 | 14 | US-10-060-102-14 |
| 8 | 77 | 97.5 | 16 | 15 | US-10-721-839-14 |
| 9 | 77 | 97.5 | 16 | 9 | US-09-840-009-2 |
| 10 | 77 | 97.5 | 16 | 9 | US-09-840-009-9 |
| 11 | 77 | 97.5 | 16 | 9 | US-09-840-009-16 |
| 12 | 77 | 97.5 | 16 | 9 | US-09-840-009-23 |
| 13 | 77 | 97.5 | 16 | 9 | US-09-840-009-30 |

| | | | | | | |
|----|----|------|----|----|------------------|--------------------|
| 14 | 77 | 97.5 | 18 | 14 | US-10-060-102-9 | Sequence 9, Appl1 |
| 15 | 77 | 97.5 | 18 | 14 | US-10-060-102-12 | Sequence 12, Appl1 |
| 16 | 77 | 97.5 | 18 | 15 | US-10-721-839-9 | Sequence 9, Appl1 |
| 17 | 77 | 97.5 | 18 | 15 | US-10-721-839-12 | Sequence 12, Appl1 |
| 18 | 77 | 97.5 | 29 | 15 | US-10-060-102-8 | Sequence 8, Appl1 |
| 19 | 77 | 97.5 | 29 | 15 | US-10-721-839-8 | Sequence 8, Appl1 |
| 20 | 72 | 91.1 | 18 | 9 | US-09-840-009-4 | Sequence 4, Appl1 |
| 21 | 72 | 91.1 | 18 | 9 | US-09-840-009-8 | Sequence 8, Appl1 |
| 22 | 72 | 91.1 | 18 | 9 | US-09-840-009-11 | Sequence 11, Appl1 |
| 23 | 72 | 91.1 | 18 | 9 | US-09-840-009-15 | Sequence 15, Appl1 |
| 24 | 72 | 91.1 | 18 | 9 | US-09-840-009-18 | Sequence 18, Appl1 |
| 25 | 72 | 91.1 | 18 | 9 | US-09-840-009-22 | Sequence 22, Appl1 |
| 26 | 72 | 91.1 | 18 | 9 | US-09-840-009-25 | Sequence 25, Appl1 |
| 27 | 72 | 91.1 | 18 | 9 | US-09-840-009-29 | Sequence 29, Appl1 |
| 28 | 72 | 91.1 | 18 | 14 | US-10-060-102-25 | Sequence 25, Appl1 |
| 29 | 72 | 91.1 | 18 | 15 | US-10-721-839-25 | Sequence 25, Appl1 |
| 30 | 71 | 89.9 | 18 | 9 | US-09-840-009-5 | Sequence 5, Appl1 |
| 31 | 71 | 89.9 | 18 | 9 | US-09-840-009-12 | Sequence 12, Appl1 |
| 32 | 71 | 89.9 | 18 | 9 | US-09-840-009-19 | Sequence 19, Appl1 |
| 33 | 71 | 89.9 | 18 | 9 | US-09-840-009-26 | Sequence 26, Appl1 |
| 34 | 70 | 88.6 | 18 | 9 | US-09-840-009-6 | Sequence 6, Appl1 |
| 35 | 70 | 88.6 | 18 | 9 | US-09-840-009-7 | Sequence 7, Appl1 |
| 36 | 70 | 88.6 | 18 | 9 | US-09-840-009-13 | Sequence 13, Appl1 |
| 37 | 70 | 88.6 | 18 | 9 | US-09-840-009-14 | Sequence 14, Appl1 |
| 38 | 70 | 88.6 | 18 | 9 | US-09-840-009-20 | Sequence 20, Appl1 |
| 39 | 70 | 88.6 | 18 | 9 | US-09-840-009-21 | Sequence 21, Appl1 |
| 40 | 70 | 88.6 | 18 | 9 | US-09-840-009-27 | Sequence 27, Appl1 |
| 41 | 70 | 88.6 | 18 | 9 | US-09-840-009-28 | Sequence 28, Appl1 |
| 42 | 69 | 87.3 | 18 | 9 | US-09-840-009-3 | Sequence 3, Appl1 |
| 43 | 69 | 87.3 | 18 | 9 | US-09-840-009-10 | Sequence 10, Appl1 |
| 44 | 69 | 87.3 | 18 | 9 | US-09-840-009-17 | Sequence 17, Appl1 |
| 45 | 69 | 87.3 | 18 | 9 | US-09-840-009-24 | Sequence 24, Appl1 |

ALIGNMENTS

RESULT 1
US-10-060-102-15
; Sequence 15, Application US/10060102
; Publication No. US20030022829A1
GENERAL INFORMATION:
; APPLICANT: MAURY, WENDY
; APPLICANT: STAPLETON, JACK
; APPLICANT: ROLLER, RICHARD
; APPLICANT: STINSKI, MARK
; APPLICANT: MCCRAY, PAUL B.
; APPLICANT: TRACK, BRIAN
; TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMAL
; FILE REFERENCE: IOWA:035US
; CURRENT APPLICATION NUMBER: US/10/060,102
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 60/309,368
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/265,270
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-060-102-15

Query Match 100.0%; Score 79; DB 14; Length 16;
Best Local Similarity 100.0%; Pred. No. 1,1e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 1 NRRIRKIHIIKKY 16

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:18:40 ; Search time 15.1955 Seconds

(without alignments)
78.601 Million cell updates/sec

Title: US-09-642-744d-10

Perfect score: 79

Sequence: 1 NRRIRKIHIIKKY 16

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
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6: /cgn2_6/prodata/1/iaa/5B_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 1 | 77 | 97.5 | 18 | US-09-840-009-2 | Sequence 2, Appl |
| 2 | 77 | 97.5 | 18 | US-09-840-009-9 | Sequence 9, Appl |
| 3 | 77 | 97.5 | 18 | US-09-840-009-16 | Sequence 16, Appl |
| 4 | 77 | 97.5 | 18 | US-09-840-009-23 | Sequence 23, Appl |
| 5 | 77 | 97.5 | 18 | US-09-840-009-30 | Sequence 30, Appl |
| 6 | 72 | 91.1 | 18 | US-09-840-009-4 | Sequence 4, Appl |
| 7 | 72 | 91.1 | 18 | US-09-840-009-8 | Sequence 8, Appl |
| 8 | 72 | 91.1 | 18 | US-09-840-009-11 | Sequence 11, Appl |
| 9 | 72 | 91.1 | 18 | US-09-840-009-15 | Sequence 15, Appl |
| 10 | 72 | 91.1 | 18 | US-09-840-009-18 | Sequence 18, Appl |
| 11 | 72 | 91.1 | 18 | US-09-840-009-22 | Sequence 22, Appl |
| 12 | 72 | 91.1 | 18 | US-09-840-009-25 | Sequence 25, Appl |
| 13 | 72 | 91.1 | 18 | US-09-840-009-29 | Sequence 29, Appl |
| 14 | 72 | 91.1 | 18 | US-09-840-009-3 | Sequence 3, Appl |
| 15 | 71 | 89.9 | 18 | US-09-840-009-5 | Sequence 5, Appl |
| 16 | 71 | 89.9 | 18 | US-09-840-009-12 | Sequence 12, Appl |
| 17 | 71 | 89.9 | 18 | US-09-840-009-19 | Sequence 19, Appl |
| 18 | 71 | 89.9 | 18 | US-09-840-009-26 | Sequence 26, Appl |
| 19 | 70 | 88.6 | 18 | US-09-840-009-7 | Sequence 7, Appl |
| 20 | 70 | 88.6 | 18 | US-09-840-009-13 | Sequence 13, Appl |
| 21 | 70 | 88.6 | 18 | US-09-840-009-14 | Sequence 14, Appl |
| 22 | 70 | 88.6 | 18 | US-09-840-009-20 | Sequence 20, Appl |
| 23 | 70 | 88.6 | 18 | US-09-840-009-21 | Sequence 21, Appl |
| 24 | 70 | 88.6 | 18 | US-09-840-009-27 | Sequence 27, Appl |
| 25 | 69 | 87.3 | 18 | US-09-840-009-28 | Sequence 28, Appl |
| 26 | 69 | 87.3 | 18 | US-09-840-009-3 | Sequence 3, Appl |
| 27 | 69 | 87.3 | 18 | US-09-840-009-10 | Sequence 10, Appl |

| | | | | | |
|----|----|------|-----|----------------------|--------------------|
| 28 | 69 | 87.3 | 18 | US-09-840-009-17 | Sequence 17, Appl |
| 29 | 69 | 87.3 | 18 | US-09-840-009-24 | Sequence 24, Appl |
| 30 | 69 | 87.3 | 18 | US-09-840-009-31 | Sequence 31, Appl |
| 31 | 63 | 79.7 | 18 | US-09-840-009-34 | Sequence 34, Appl |
| 32 | 63 | 79.7 | 18 | US-09-840-009-35 | Sequence 35, Appl |
| 33 | 61 | 77.2 | 18 | US-09-840-009-32 | Sequence 32, Appl |
| 34 | 61 | 77.2 | 18 | US-09-840-009-33 | Sequence 33, Appl |
| 35 | 57 | 72.2 | 18 | US-09-840-009-1 | Sequence 1, Appl |
| 36 | 55 | 69.6 | 18 | US-09-840-009-36 | Sequence 36, Appl |
| 37 | 55 | 69.6 | 18 | US-09-840-009-37 | Sequence 37, Appl |
| 38 | 47 | 59.5 | 160 | US-09-917-340-36 | Sequence 36, Appl |
| 39 | 47 | 59.5 | 169 | US-09-270-767-35406 | Sequence 35406, A |
| 40 | 47 | 59.5 | 169 | US-09-270-767-350623 | Sequence 350623, A |
| 41 | 43 | 54.4 | 66 | US-09-270-767-39626 | Sequence 39626, A |
| 42 | 43 | 54.4 | 66 | US-09-270-767-54843 | Sequence 54843, A |
| 43 | 42 | 53.2 | 24 | US-09-785-0598-5 | Sequence 5, Appl |
| 44 | 42 | 53.2 | 36 | US-09-785-0598-6 | Sequence 6, Appl |
| 45 | 42 | 53.2 | 42 | US-09-785-0598-7 | Sequence 7, Appl |

ALIGNMENTS

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RESULT 1
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; Sequence 2, Application US/09840009
; Patent No. 6492328
; GENERAL INFORMATION:
; APPLICANT: Lehner, Robert I.
; APPLICANT: Waring, Alan J.
; TITLE OF INVENTION: NOVISPIRINS: ANTIMICROBIAL PEPTIDES
; FILE REFERENCE: 06510-1950
; CURRENT APPLICATION NUMBER: US/09/840,009
; PRIOR FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 09/606,858
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic antimicrobial peptide
US-09-840-009-2
Query Match          97.5%; Score 77; DB 4; Length 18;
Best Local Similarity 93.8%; Pred. No. 1.5e-05;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Oy 1 NRRIRKIHIIKKY 16
Db 2 NRRIRKIHIIKKY 17
RESULT 2
US-09-840-009-9
; Sequence 9, Application US/09840009
; Patent No. 6492328
; GENERAL INFORMATION:
; APPLICANT: Lehner, Robert I.
; APPLICANT: Waring, Alan J.
; TITLE OF INVENTION: NOVISPIRINS: ANTIMICROBIAL PEPTIDES
; FILE REFERENCE: 06510-1950
; CURRENT APPLICATION NUMBER: US/09/840,009
; PRIOR FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 09/606,858
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
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OM protein - protein search, using SW model

Run on: May 2, 2005, 12:17:55; Search time 56.0894 Seconds
(without alignments)
110.327 Million cell updates/sec

Title: US-09-642-744D-10

Perfect score: 79

Sequence: 1 NRRIRKIHIMKY 16

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: A_Geneseq_16Dec04:*

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 2 | 79 | 100.0 | 16 | 5 | ABP53282 |
| 3 | 79 | 100.0 | 18 | 4 | AAAB70654 |
| 4 | 79 | 100.0 | 18 | 5 | ABP53278 |
| 5 | 79 | 100.0 | 18 | 5 | ABP53277 |
| 6 | 79 | 100.0 | 20 | 4 | AAAB70653 |
| 7 | 77 | 97.5 | 16 | 4 | AAAB70656 |
| 8 | 77 | 97.5 | 16 | 5 | ABP53281 |
| 9 | 77 | 97.5 | 18 | 4 | AAAB70655 |
| 10 | 77 | 97.5 | 18 | 4 | AAAB70648 |
| 11 | 77 | 97.5 | 18 | 5 | AAE20882 |
| 12 | 77 | 97.5 | 18 | 5 | AAE20875 |
| 13 | 77 | 97.5 | 18 | 5 | AAE20854 |
| 14 | 77 | 97.5 | 18 | 5 | AAE20861 |
| 15 | 77 | 97.5 | 18 | 5 | AAE20868 |
| 16 | 77 | 97.5 | 18 | 5 | ABP53276 |
| 17 | 77 | 97.5 | 18 | 5 | ABP53279 |
| 18 | 77 | 97.5 | 29 | 4 | AAAB70675 |
| 19 | 77 | 97.5 | 29 | 5 | ABP53275 |
| 20 | 72 | 91.1 | 18 | 5 | AAE20870 |
| 21 | 72 | 91.1 | 18 | 5 | AAE20860 |
| 22 | 72 | 91.1 | 18 | 5 | AAE20881 |
| 23 | 72 | 91.1 | 18 | 5 | AAE20867 |
| 24 | 72 | 91.1 | 18 | 5 | AAE20874 |
| 25 | 72 | 91.1 | 18 | 5 | AAE20863 |

ALIGNMENTS

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| 26 | 72 | 91.1 | 18 | 5 | AAE20877 | AAe20877 T11-nov1s |
| 27 | 72 | 91.1 | 18 | 5 | AAE20856 | AAe20856 T6-nov1sp |
| 28 | 72 | 91.1 | 18 | 5 | ABP53292 | ABp53292 Synthetic |
| 29 | 71 | 89.9 | 18 | 5 | AAE20864 | AAe20864 S7-nov1sp |
| 30 | 71 | 89.9 | 18 | 5 | AAE20871 | AAe20871 S10-nov1s |
| 31 | 71 | 89.9 | 18 | 5 | AAE20878 | AAe20878 S11-nov1s |
| 32 | 71 | 89.9 | 18 | 5 | AAE20857 | AAe20857 S6-nov1sp |
| 33 | 70 | 88.6 | 18 | 5 | AAE20872 | AAe20872 G10-nov1s |
| 34 | 70 | 88.6 | 18 | 5 | AAE20873 | AAe20873 G10-nov1s |
| 35 | 70 | 88.6 | 18 | 5 | AAE20858 | AAe20858 G6-nov1sp |
| 36 | 70 | 88.6 | 18 | 5 | AAE20866 | AAe20866 D7-nov1sp |
| 37 | 70 | 88.6 | 18 | 5 | AAE20879 | AAe20879 E11-nov1s |
| 38 | 70 | 88.6 | 18 | 5 | AAE20865 | AAe20865 E7-nov1sp |
| 39 | 70 | 88.6 | 18 | 5 | AAE20880 | AAe20880 D11-nov1s |
| 40 | 70 | 88.6 | 18 | 5 | AAE20859 | AAe20859 D6-nov1sp |
| 41 | 69 | 87.3 | 18 | 5 | AAE20862 | AAe20862 G7-nov1sp |
| 42 | 69 | 87.3 | 18 | 5 | AAE20876 | AAe20876 G11-nov1s |
| 43 | 69 | 87.3 | 18 | 5 | AAE20863 | AAe20863 G10-nov1s |
| 44 | 69 | 87.3 | 18 | 5 | AAE20869 | AAe20869 G10-nov1s |
| 45 | 69 | 87.3 | 18 | 5 | AAE20855 | AAe20855 G6-nov1sp |

RESULT 1
AAAB70657
ID AAAB70657 standard; peptide; 16 AA.

AC AAAB70657;
DT 15-MAY-2001 (first entry)

DE Ovine SMAAP 29 cathelicidin derived antimicrobial peptide SEQ ID NO:10.
XX Ovine; SMAAP29; lupine; RCAP 18; cathelicidin; antimicrobial;
XX bactericidal; antibiotic; antiviral; microbial growth inhibitor;
XX proliferation inhibitor; gene therapy; Pseudomonas aeruginosa;
XX Burkholderia cepacia; Alcaligenes; Xanthomonas.

OS Ovis aries.

PN WO200112668-A1.

PD 22-FEB-2001.

PF 18-AUG-2000; 2000WO-US022781.

PR 18-AUG-1999; 99US-0149886P.

PA (IOWA) UNIV IOWA RES FOUND.
(REGC) UNIV CALIFORNIA.

PI Tack BE, Mccrery P, Welsh M, Travis SM, Lehrer R;

DR WPI; 2001-234911/24.

PT New antimicrobial peptides useful as antibiotics for inhibiting growth
and proliferation of microbes, and for treating microbial infections.

PS Claim 1, Page 103; 137p; English.

XX AAAB70648 to AAAB70675 represent antimicrobial peptides (I), of which
CC AAAB70648 to AAAB70664, AAAB70674 and AAAB70675 are derived from the ovine
CC SMAAP 29 cathelicidin family peptide, and AAAB70665 to AAAB70673 are derived
CC from the lupine RCAP 18 cathelicidin family peptide. (I) have antibiotic,
CC antimicrobial and antiviral activities, and can be used as microbial
CC growth and proliferation inhibitors, and in gene therapy. (II) are useful
CC for inhibiting microbial growth in an environment capable of sustaining
CC such growth, for inhibiting microbial growth or strain in a host, and
CC inhibiting the growth of drug-resistant microbial strains such as
XX Pseudomonas aeruginosa, Burkholderia cepacia, Alcaligenes and Xanthomonas

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:17:06 ; Search time 49.9218 Seconds

(without alignments)
164.122 Million cell updates/sec

Title: US-09-642-744D-9

Sequence: 1 NLRRIKRIHIKY 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|-------|-------------|--------|----|------------|--------------------|
| 1 | 49 | 62.0 | 160 | 1 | SCS1_SHEEP | P49928 ovls arles |
| 2 | 49 | 62.0 | 160 | 1 | SCS2_SHEEP | P49929 ovls arles |
| 3 | 48 | 60.8 | 500 | 1 | TF3B_SCHPO | O96670 schizosacch |
| 4 | 46 | 58.2 | 349 | 2 | O736DS | O736DS bacillus ce |
| 5 | 46 | 58.2 | 349 | 2 | O81P89 | O81P89 bacillus an |
| 6 | 46 | 58.2 | 349 | 2 | O6HH12 | O6HH12 bacillus th |
| 7 | 45 | 57.0 | 308 | 2 | O8R2C7 | O8R2C7 mus musculi |
| 8 | 45 | 57.0 | 402 | 2 | O8H143 | O8H143 plasmodium |
| 9 | 44 | 55.7 | 834 | 2 | O7RR10 | O7RR10 plasmodium |
| 10 | 44 | 55.7 | 684 | 2 | O7GNN1 | O7GNN1 giardia lam |
| 11 | 44 | 55.7 | 954 | 2 | O9GQ15 | O9GQ15 giardia lam |
| 12 | 44 | 55.7 | 969 | 2 | O9U022 | O9U022 giardia lam |
| 13 | 44 | 55.7 | 1137 | 2 | O6LF77 | O6LF77 plasmodium |
| 14 | 43.5 | 55.1 | 313 | 2 | O8CNR3 | O8CNR3 staphylococ |
| 15 | 43 | 54.4 | 146 | 2 | O9A1H3 | O9A1H3 carsonella |
| 16 | 43 | 54.4 | 182 | 2 | O896E1 | O896E1 clostridium |
| 17 | 43 | 54.4 | 234 | 2 | O59264 | O59264 clostridium |
| 18 | 43 | 54.4 | 250 | 2 | O6LF79 | O6LF79 plasmodium |
| 19 | 43 | 54.4 | 537 | 2 | O97W16 | O97W16 sulfolobus |
| 20 | 43 | 54.4 | 638 | 2 | O8D796 | O8D796 vibrio vuln |
| 21 | 43 | 54.4 | 660 | 2 | O7W6A0 | O7W6A0 vibrio vuln |
| 22 | 43 | 54.4 | 821 | 1 | MCW6_HUMAN | O15566 homo sapien |
| 23 | 43 | 54.4 | 840 | 2 | O9DHN4 | O9DHN4 yaba-like d |
| 24 | 43 | 54.4 | 875 | 2 | O8R8R4 | O8R8R4 thermospora |
| 25 | 43 | 54.4 | 878 | 2 | O7RY40 | O7RY40 neurospora |
| 26 | 42.5 | 53.8 | 3267 | 2 | O81BZ0 | O81BZ0 anophelis g |
| 27 | 42 | 53.2 | 301 | 2 | O7Q4C0 | O7Q4C0 anophelis g |
| 28 | 42 | 53.2 | 125 | 2 | O9AVZ1 | O9AVZ1 guilardina |
| 29 | 42 | 53.2 | 146 | 1 | RUVX MYCPU | O99Q13 mycoplasma |
| 30 | 42 | 53.2 | 198 | 2 | O6L1E8 | O6L1E8 picophilus |
| 31 | 42 | 53.2 | 231 | 2 | O8RAG4 | O8RAG4 thermospora |

| | | | | | | |
|----|------|------|------|---|------------|--------------------|
| 32 | 42 | 53.2 | 233 | 2 | O9L7X2 | O9L7X2 clostridium |
| 33 | 42 | 53.2 | 233 | 2 | O8XJ18 | O8XJ18 clostridium |
| 34 | 42 | 53.2 | 234 | 2 | O95ZM1 | O95ZM1 caenorhabdi |
| 35 | 42 | 53.2 | 420 | 1 | PR11_HUMAN | P49642 homo sapien |
| 36 | 42 | 53.2 | 460 | 2 | O9VJ03 | O9VJ03 drosophila |
| 37 | 42 | 53.2 | 507 | 1 | MCW6_RAT | O62724 rattus norv |
| 38 | 42 | 53.2 | 549 | 2 | O81PC2 | O81PC2 drosophila |
| 39 | 42 | 53.2 | 561 | 2 | O6EBB6 | O6EBB6 campylobact |
| 40 | 42 | 53.2 | 1279 | 2 | O8IB12 | O8IB12 plasmodium |
| 41 | 42 | 53.2 | 2084 | 2 | O81J16 | O81J16 plasmodium |
| 42 | 42 | 53.2 | 6077 | 2 | O6LPH6 | O6LPH6 plasmodium |
| 43 | 41.5 | 52.5 | 313 | 2 | O8NVV6 | O8NVV6 staphylococ |
| 44 | 41.5 | 52.5 | 313 | 2 | O53606 | O53606 staphylococ |
| 45 | 41.5 | 52.5 | 313 | 2 | O7A2Q3 | O7A2Q3 staphylococ |

ALIGNMENTS

RESULT 1
ID SCS1_SHEEP STANDARD; PRT; 160 AA.
AC P49928;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Cathelin-related peptide SCS precursor 1 (Antibacterial peptide SWAP-29)
DE 29) (Myeloid antibacterial peptide SWAP-29).
OS Ovis aries (Sheep).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RX MEDLINE=96140581; PubMed=8549789; DOI=10.1016/0014-5793(95)01390-3;
RA Mahoney M.M., Lee A.Y., Brezinski-Caliguri D.J., Huttner K.M.;
RT "Molecular analysis of the sheep cathelin family reveals a novel
antimicrobial peptide.";
RT FEBS Lett. 377:519-522 (1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Huttner K.M., Mahoney M.M.;
RT Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Thermolabile, broad spectrum, bactericidal agent.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the cathelicidin family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See <http://www.ebi.ac.uk/announcements>
CC or send an email to license@ebi.ac.uk).
CC
CC -----
CC EMBL: X92757; CAA63412.1; -
CC EMBL: U60600; AAB49715.1; -
CC PDB: 1FRR; NMR: A-132-160.
CC InterPro: IPR001894; Cathelicidin.
CC Pfam: PF00666; Cathelicidins; 1.
CC ProDom: PD001838; Cathelicidins; 1.
CC PROSITE: PS00946; CATHELICIDINS_1; 1.
CC PROSITE: PS00947; CATHELICIDINS_2; 1.
CC 3D-structure: Antibiotic; Pyrrolidone carboxylic acid; Signal.
CC SIGNAL 1 29
CC PROPEP 30 131
CC PEPTIDE 132 160
CC MOD_RSS 30 30
CC FT
CC FT
CC FT
CC DISULFID 86 97
CC By similarity.
CC Cathelin-related peptide SCS.
CC Pyrrolidone carboxylic acid (by
CC similarity).
CC By similarity.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:21:40 / Search time 9.92179 Seconds

(without alignments)
155.160 Million cell updates/sec

Title: US-09-642-744D-9

Perfect score: 79

Sequence: 1 NRRIIRKIHIIKXY 16

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|----------------------|
| 1 | 49 | 62.0 | 152 | 2 S68411 | cathelin-related p |
| 2 | 49 | 62.0 | 160 | 2 S68412 | cathelin-related p |
| 3 | 49 | 62.0 | 160 | 2 S68228 | myeloid antimicrob |
| 4 | 43 | 54.4 | 234 | 2 D97108 | DNA-dependent RNA |
| 5 | 43 | 54.4 | 234 | 2 I40822 | sigk protein - Clo |
| 6 | 43 | 54.4 | 537 | 2 C90389 | conserved hypochet |
| 7 | 42 | 53.2 | 125 | 2 A99114 | hypothetical prote |
| 8 | 42 | 53.2 | 146 | 2 D90581 | conserved hypochet |
| 9 | 42 | 53.2 | 420 | 2 S45630 | DNA primase chain |
| 10 | 42 | 53.2 | 507 | 2 T10753 | interstitial DNA rep |
| 11 | 42 | 53.2 | 1741 | 2 T15978 | hypothetical prote |
| 12 | 41.5 | 52.5 | 313 | 2 A89971 | cmp-binding-factor |
| 13 | 41 | 51.9 | 41 | 2 S77768 | hypothetical prote |
| 14 | 41 | 51.9 | 186 | 2 B90116 | hypothetical prote |
| 15 | 41 | 51.9 | 337 | 2 S46010 | hypothetical prote |
| 16 | 41 | 51.9 | 414 | 2 G64091 | cell division prot |
| 17 | 41 | 51.9 | 417 | 2 A33269 | DNA primase (BC 2. |
| 18 | 41 | 51.9 | 483 | 2 S75369 | hypothetical prote |
| 19 | 41 | 51.9 | 613 | 2 F64056 | probable ATP-depen |
| 20 | 41 | 51.9 | 867 | 2 G69485 | DNA-directed RNA p |
| 21 | 40.5 | 51.3 | 381 | 1 C64416 | conserved hypochet |
| 22 | 40 | 50.6 | 105 | 2 F71128 | hypothetical prote |
| 23 | 40 | 50.6 | 189 | 2 H96903 | transcription regu |
| 24 | 40 | 50.6 | 370 | 2 C70464 | GTP-binding protei |
| 25 | 40 | 50.6 | 552 | 2 B90749 | hypothetical prote |
| 26 | 40 | 50.6 | 552 | 2 F85599 | hypothetical prote |
| 27 | 40 | 50.6 | 552 | 2 D64826 | YbD protein - Bac |
| 28 | 40 | 50.6 | 1634 | 2 B64410 | DNA-directed RNA p |
| 29 | 39 | 49.4 | 113 | 2 G90223 | DNA-directed RNA p |

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| 30 | 39 | 49.4 | 156 | 1 D71689 | hypothetical prote |
| 31 | 39 | 49.4 | 202 | 1 H70318 | conserved hypochet |
| 32 | 39 | 49.4 | 210 | 2 AC1577 | precursor isomeras |
| 33 | 39 | 49.4 | 292 | 2 A97035 | cation efflux syst |
| 34 | 39 | 49.4 | 319 | 1 S19248 | RNA-directed DNA p |
| 35 | 39 | 49.4 | 334 | 2 B72301 | endoglucanase - Th |
| 36 | 39 | 49.4 | 391 | 2 B82360 | cell division prot |
| 37 | 39 | 49.4 | 407 | 2 T37888 | hypothetical prote |
| 38 | 39 | 49.4 | 463 | 2 B82160 | hypothetical prote |
| 39 | 39 | 49.4 | 782 | 2 S56141 | HAK1 protein - Yea |
| 40 | 38 | 48.1 | 87 | 2 S00180 | spermatid protein |
| 41 | 38 | 48.1 | 102 | 2 AD1420 | PTS cellulobiose-spe |
| 42 | 38 | 48.1 | 102 | 2 AE1795 | PTS cellulobiose-spe |
| 43 | 38 | 48.1 | 172 | 2 T28288 | ORF MSY127 hypothe |
| 44 | 38 | 48.1 | 177 | 2 T28362 | hypothetical prote |
| 45 | 38 | 48.1 | 197 | 2 A90594 | holliday junction |

ALIGNMENTS

RESULT 1

S68411
cathelin-related protein 2 precursor - sheep (fragment)

C/Spectrum: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C/Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000

C/Accession: S68411

R/Mahoney, M.M.; Lee, A.Y.; Brezniski-Calliguri, D.J.; Huttner, K.M.

A/Title: Molecular analysis of the sheep cathelin family reveals a novel antimicrobial

A/Reference number: S68411; PMID:96140581; PMID:8549789

A/Accession: S68411

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-152 <MAH>

A/Cross-references: EMBL:X92757

C/Genetics:

C/Superfamily: cathelin; cystatin homology

F/1-21/Domain: signal sequence #status predicted <SIG>

F/14-123/Domain: cystatin homology <CYS>

F/21-123/Domain: propeptide #status predicted <PRO>

F/124-152/Product: cathelin-related protein 2 #status predicted <MAT>

Query Match Best local similarity 62.0%; Score 49; DB 2; Length 152;

Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 LRRIRKIHIIKXY 16

Db 126 LRRIRKIHIIKXY 140

RESULT 2

S68412
cathelin-related protein 1 precursor - sheep

C/Spectrum: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C/Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000

C/Accession: S68412

R/Mahoney, M.M.; Lee, A.Y.; Brezniski-Calliguri, D.J.; Huttner, K.M.

A/Title: Molecular analysis of the sheep cathelin family reveals a novel antimicrobial

A/Reference number: S68411; PMID:96140581; PMID:8549789

A/Accession: S68412

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-160 <MAH>

A/Cross-references: EMBL:X92758

hypothetical prote
conserved hypochet
precursor isomeras
cation efflux syst
RNA-directed DNA p
endoglucanase - Th
cell division prot
hypothetical prote
hypothetical prote
HAK1 protein - Yea
spermatid protein
PTS cellulobiose-spe
PTS cellulobiose-spe
ORF MSY127 hypothe
hypothetical prote
holliday junction

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OM protein - protein search, using sw model

Run on: May 2, 2005, 13:03:56 ; Search time 43.5307 Seconds

(without alignments)
122.435 Million cell updates/sec

Title: US-09-642-744D-9

Sequence: 1 NLRRIKIHIIKKY 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1426032 seqs, 333106140 residues

Total number of hits satisfying chosen parameters: 1426032

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:
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2: /cgn2_6/ptodata/1/pubppa/PCT_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 2 | 79 | 100.0 | 16 | 15 US-10-721-839-14 | Sequence 14, Appl |
| 3 | 79 | 100.0 | 18 | 9 US-09-840-009-2 | Sequence 2, Appl |
| 4 | 79 | 100.0 | 18 | 9 US-09-840-009-9 | Sequence 9, Appl |
| 5 | 79 | 100.0 | 18 | 9 US-09-840-009-16 | Sequence 16, Appl |
| 6 | 79 | 100.0 | 18 | 9 US-09-840-009-23 | Sequence 23, Appl |
| 7 | 79 | 100.0 | 18 | 9 US-09-840-009-30 | Sequence 30, Appl |
| 8 | 79 | 100.0 | 18 | 14 US-10-060-102-9 | Sequence 9, Appl |
| 9 | 79 | 100.0 | 18 | 14 US-10-060-102-12 | Sequence 12, Appl |
| 10 | 79 | 100.0 | 18 | 15 US-10-721-839-9 | Sequence 9, Appl |
| 11 | 79 | 100.0 | 18 | 15 US-10-721-839-12 | Sequence 12, Appl |
| 12 | 79 | 100.0 | 29 | 14 US-10-060-102-8 | Sequence 8, Appl |
| 13 | 79 | 100.0 | 29 | 15 US-10-721-839-8 | Sequence 8, Appl |

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|----|----|------|----|----|------------------|-------------------|
| 14 | 77 | 97.5 | 16 | 14 | US-10-060-102-15 | Sequence 15, Appl |
| 15 | 77 | 97.5 | 16 | 15 | US-10-721-839-15 | Sequence 15, Appl |
| 16 | 77 | 97.5 | 18 | 14 | US-10-060-102-10 | Sequence 10, Appl |
| 17 | 77 | 97.5 | 18 | 14 | US-10-060-102-11 | Sequence 11, Appl |
| 18 | 77 | 97.5 | 18 | 15 | US-10-721-839-10 | Sequence 10, Appl |
| 19 | 77 | 97.5 | 18 | 15 | US-10-721-839-11 | Sequence 11, Appl |
| 20 | 74 | 93.7 | 18 | 9 | US-09-840-009-4 | Sequence 4, Appl |
| 21 | 74 | 93.7 | 18 | 9 | US-09-840-009-8 | Sequence 8, Appl |
| 22 | 74 | 93.7 | 18 | 9 | US-09-840-009-11 | Sequence 11, Appl |
| 23 | 74 | 93.7 | 18 | 9 | US-09-840-009-15 | Sequence 15, Appl |
| 24 | 74 | 93.7 | 18 | 9 | US-09-840-009-18 | Sequence 18, Appl |
| 25 | 74 | 93.7 | 18 | 9 | US-09-840-009-22 | Sequence 22, Appl |
| 26 | 74 | 93.7 | 18 | 9 | US-09-840-009-25 | Sequence 25, Appl |
| 27 | 74 | 93.7 | 18 | 9 | US-09-840-009-29 | Sequence 29, Appl |
| 28 | 74 | 93.7 | 18 | 14 | US-10-060-102-25 | Sequence 25, Appl |
| 29 | 74 | 93.7 | 18 | 15 | US-10-721-839-25 | Sequence 25, Appl |
| 30 | 73 | 92.4 | 18 | 9 | US-09-840-009-5 | Sequence 5, Appl |
| 31 | 73 | 92.4 | 18 | 9 | US-09-840-009-12 | Sequence 12, Appl |
| 32 | 73 | 92.4 | 18 | 9 | US-09-840-009-19 | Sequence 19, Appl |
| 33 | 73 | 92.4 | 18 | 9 | US-09-840-009-26 | Sequence 26, Appl |
| 34 | 72 | 91.1 | 18 | 9 | US-09-840-009-6 | Sequence 6, Appl |
| 35 | 72 | 91.1 | 18 | 9 | US-09-840-009-7 | Sequence 7, Appl |
| 36 | 72 | 91.1 | 18 | 9 | US-09-840-009-13 | Sequence 13, Appl |
| 37 | 72 | 91.1 | 18 | 9 | US-09-840-009-14 | Sequence 14, Appl |
| 38 | 72 | 91.1 | 18 | 9 | US-09-840-009-20 | Sequence 20, Appl |
| 39 | 72 | 91.1 | 18 | 9 | US-09-840-009-21 | Sequence 21, Appl |
| 40 | 72 | 91.1 | 18 | 9 | US-09-840-009-27 | Sequence 27, Appl |
| 41 | 72 | 91.1 | 18 | 9 | US-09-840-009-28 | Sequence 28, Appl |
| 42 | 71 | 89.9 | 18 | 9 | US-09-840-009-3 | Sequence 3, Appl |
| 43 | 71 | 89.9 | 18 | 9 | US-09-840-009-10 | Sequence 10, Appl |
| 44 | 71 | 89.9 | 18 | 9 | US-09-840-009-17 | Sequence 17, Appl |
| 45 | 71 | 89.9 | 18 | 9 | US-09-840-009-24 | Sequence 24, Appl |

ALIGNMENTS

RESULT 1
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; Sequence 14, Application US/10060102
; Publication No. US20030022829A1
; GENERAL INFORMATION:
; APPLICANT: MAURY, WENDY
; APPLICANT: STAPLETON, JACK
; APPLICANT: ROLLER, RICHARD
; APPLICANT: STINSKI, MARK
; APPLICANT: MCCRAY, PAUL B.
; TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMAL
; FILE REFERENCE: IOWA:03US
; CURRENT APPLICATION NUMBER: US/10/060,102
; PRIOR FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 60/305,368
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/265,270
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 14
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-060-102-14

Query Match 100.0%; Score 79; DB 14; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 NLRRIKIHIIKKY 16

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:18:40 ; Search time 15.1955 Seconds

(without alignments)
78.601 Million cell updates/sec

Title: US-09-642-744D-9
Perfect score: 79
Sequence: 1 NLRRIKIHIIKKY 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 2 | 79 | 100.0 | 18 | 4 | US-09-840-009-9 |
| 3 | 79 | 100.0 | 18 | 4 | US-09-840-009-16 |
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| 5 | 79 | 100.0 | 18 | 4 | US-09-840-009-30 |
| 6 | 74 | 93.7 | 18 | 4 | US-09-840-009-4 |
| 7 | 74 | 93.7 | 18 | 4 | US-09-840-009-8 |
| 8 | 74 | 93.7 | 18 | 4 | US-09-840-009-11 |
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| 19 | 72 | 91.1 | 18 | 4 | US-09-840-009-7 |
| 20 | 72 | 91.1 | 18 | 4 | US-09-840-009-13 |
| 21 | 72 | 91.1 | 18 | 4 | US-09-840-009-14 |
| 22 | 72 | 91.1 | 18 | 4 | US-09-840-009-20 |
| 23 | 72 | 91.1 | 18 | 4 | US-09-840-009-21 |
| 24 | 72 | 91.1 | 18 | 4 | US-09-840-009-27 |
| 25 | 72 | 91.1 | 18 | 4 | US-09-840-009-28 |
| 26 | 71 | 89.9 | 18 | 4 | US-09-840-009-3 |
| 27 | 71 | 89.9 | 18 | 4 | US-09-840-009-10 |

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| 28 | 71 | 89.9 | 18 | 4 | US-09-840-009-17 | Sequence 17, Appl |
| 29 | 71 | 89.9 | 18 | 4 | US-09-840-009-24 | Sequence 24, Appl |
| 30 | 71 | 89.9 | 18 | 4 | US-09-840-009-31 | Sequence 31, Appl |
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| 32 | 65 | 82.3 | 18 | 4 | US-09-840-009-35 | Sequence 35, Appl |
| 33 | 63 | 79.7 | 18 | 4 | US-09-840-009-32 | Sequence 32, Appl |
| 34 | 63 | 79.7 | 18 | 4 | US-09-840-009-33 | Sequence 33, Appl |
| 35 | 59 | 74.7 | 18 | 4 | US-09-840-009-1 | Sequence 1, Appl |
| 36 | 57 | 72.2 | 18 | 4 | US-09-840-009-36 | Sequence 36, Appl |
| 37 | 57 | 72.2 | 18 | 4 | US-09-840-009-37 | Sequence 37, Appl |
| 38 | 49 | 62.0 | 160 | 4 | US-09-917-340-36 | Sequence 36, Appl |
| 39 | 45 | 57.0 | 169 | 4 | US-09-270-767-35406 | Sequence 35406, A |
| 40 | 45 | 57.0 | 169 | 4 | US-09-270-767-50623 | Sequence 50623, A |
| 41 | 44 | 55.7 | 205 | 3 | US-09-134-001C-4766 | Sequence 4766, Ap |
| 42 | 43.5 | 55.1 | 167 | 4 | US-09-710-279-1502 | Sequence 1502, Ap |
| 43 | 43.5 | 55.1 | 320 | 3 | US-09-134-001C-1823 | Sequence 3823, Ap |
| 44 | 43 | 54.4 | 823 | 4 | US-09-949-016-8339 | Sequence 8339, Ap |
| 45 | 42 | 53.2 | 526 | 4 | US-09-270-767-45588 | Sequence 45588, A |

ALIGNMENTS

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RESULT 1
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; Sequence 2, Application US/09840009
; Patent No. 6492328
; GENERAL INFORMATION:
; APPLICANT: Lehner, Robert I.
; APPLICANT: Waring, Alan J.
; TITLE OF INVENTION: NOVISPIRINS: ANTIMICROBIAL PEPTIDES
; FILE REFERENCE: 06510-195W0
; CURRENT APPLICATION NUMBER: US/09/840,009
; PRIOR FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 09/606,858
; PRIOR FILING DATE: 2000-06-28
; SOFTWARE: FastSeq for Windows Version 4.0
; NUMBER OF SEQ ID NOS: 37
; SEQ ID NO 1
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic antimicrobial peptide
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Best Local Similarity 100.0%; Pred. No. 8.7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NLRRIKIHIIKKY 16
DB 2 NLRRIKIHIIKKY 17
RESULT 2
US-09-840-009-9
; Sequence 9, Application US/09840009
; Patent No. 6492328
; GENERAL INFORMATION:
; APPLICANT: Lehner, Robert I.
; APPLICANT: Waring, Alan J.
; APPLICANT: Tack, Brian F.
; TITLE OF INVENTION: NOVISPIRINS: ANTIMICROBIAL PEPTIDES
; FILE REFERENCE: 06510-195W0
; CURRENT APPLICATION NUMBER: US/09/840,009
; PRIOR FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 09/606,858
; PRIOR FILING DATE: 2000-06-28
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; SOFTWARE: FastSeq for Windows Version 4.0
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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:17:55 ; Search time 56.0894 Seconds

(without alignments)
110.327 Million cell updates/sec

Title: US-09-642-744d-9

Perfect score: 79

Sequence: 1 NLRRIKRIHIIRKY 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 4 | 79 | 100.0 | 18 | 4 AAB70648 | Aab70648 Ovine SMA |
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| 6 | 79 | 100.0 | 18 | 5 AAE20875 | Aae20875 D11-nov1 |
| 7 | 79 | 100.0 | 18 | 5 AAE20854 | Aae20854 D16-nov1 |
| 8 | 79 | 100.0 | 18 | 5 AAE20861 | Aae20861 D16-nov1 |
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| 10 | 79 | 100.0 | 18 | 5 ABP53276 | Abp53276 Synthetic |
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| 12 | 79 | 100.0 | 29 | 4 AAB70675 | Aab70675 Ovine SMA |
| 13 | 79 | 100.0 | 29 | 5 ABP53275 | Abp53275 Synthetic |
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| 18 | 77 | 97.5 | 18 | 5 ABP53277 | Abp53277 Synthetic |
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| 38 | 72 | 91.1 | 18 | 5 AAE20885 | Aae20885 E7-nov1sp |
| 39 | 72 | 91.1 | 18 | 5 AAE20880 | Aae20880 D11-nov1s |
| 40 | 72 | 91.1 | 18 | 5 AAE20859 | Aae20859 D6-nov1sp |
| 41 | 71 | 89.9 | 18 | 5 AAE20862 | Aae20862 G7-nov1sp |
| 42 | 71 | 89.9 | 18 | 5 AAE20876 | Aae20876 G11-nov1s |
| 43 | 71 | 89.9 | 18 | 5 AAE20883 | Aae20883 G10-nov1s |
| 44 | 71 | 89.9 | 18 | 5 AAE20869 | Aae20869 G10-nov1s |
| 45 | 71 | 89.9 | 18 | 5 AAE20855 | Aae20855 G6-nov1sp |

ALIGNMENTS

RESULT 1

ID AAB70656 standard; peptide; 16 AA.

XX AAB70656;

DT 15-MAY-2001 (first entry)

DE Ovine SNAP 29 cathelicidin derived antimicrobial peptide SEQ ID NO:9.

KW Ovine: SNAP29; lupine: RCAP 18; cathelicidin; antimicrobial;

KM bactericidal; antibiotic; antiviral; microbial growth inhibitor;

KW proliferation inhibitor; gene therapy; Pseudomonas aeruginosa;

KM Burkholderia cepacia; Alcaligenes; Xanthomonas.

XX Ovis aries.

OS WO200112668-A1.

PN 22-FEB-2001.

PF 18-AUG-2000; 2000WO-US022781.

PR 18-AUG-1999; 99US-0149886P.

PA (ICMA) UNIV IOWA RES FOUND.

XX (REGC) UNIV CALIFORNIA.

PI Tack BE, Mccrery P, Welsh M, Travis SM, Lehrer R;

DR WPI; 2001-234911/24.

XX New antimicrobial peptides useful as antibiotics for inhibiting growth

PT and proliferation of microbes, and for treating microbial infections.

PS Claim 1; Page 103; 137pp; English.

XX AAB70648 to AAB70675 represent antimicrobial peptides (I), of which
CC AAB70648 to AAB70674, AAB70674 and AAB70675 are derived from the ovine
CC SNAP 29 cathelicidin family peptide, and AAB70675 are derived
CC from the lupine RCAP 18 cathelicidin family peptide. (I) have antibiotic,
CC antimicrobial and antiviral activities, and can be used as microbial
CC growth and proliferation inhibitors and in gene therapy. (I) are useful
CC for inhibiting microbial growth in an environment capable of sustaining
CC such growth, for inhibiting microbial growth or strain in a host, and
CC inhibiting the growth of drug-resistant microbial strains such as
CC Pseudomonas aeruginosa, Burkholderia cepacia, Alcaligenes and Xanthomonas

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:17:06 ; Search time 56.162 Seconds

(without alignments)
164.122 Million cell updates/sec

Title: US-09-642-744D-8

Perfect score: 90

Sequence: 1 KMLRRIRKIHIIKYG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 segs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 57 | 63.3 | 160 | 1 | SCS1_SHEEP |
| 2 | 57 | 63.3 | 160 | 1 | SCS2_SHEEP |
| 3 | 54 | 60.0 | 146 | 2 | O9A1H3 |
| 4 | 50 | 55.6 | 255 | 2 | O9LJW2 |
| 5 | 49 | 54.4 | 581 | 2 | O6RBB6 |
| 6 | 48 | 53.3 | 250 | 2 | O6LFF79 |
| 7 | 48 | 53.3 | 500 | 1 | TF3B_SCHPO |
| 8 | 48 | 53.3 | 3267 | 2 | O81B20 |
| 9 | 47 | 52.2 | 113 | 2 | O703Z0 |
| 10 | 47 | 52.2 | 2017 | 2 | O675T1 |
| 11 | 46.5 | 51.7 | 314 | 2 | O651K7 |
| 12 | 46.5 | 51.7 | 324 | 2 | O62X75 |
| 13 | 46 | 51.1 | 282 | 2 | O8DYR3 |
| 14 | 46 | 51.1 | 282 | 2 | O8DYR3 |
| 15 | 46 | 51.1 | 319 | 2 | O05804 |
| 16 | 46 | 51.1 | 349 | 2 | O736D5 |
| 17 | 46 | 51.1 | 349 | 2 | O81P89 |
| 18 | 46 | 51.1 | 349 | 2 | O6H1I2 |
| 19 | 46 | 51.1 | 684 | 2 | O70NN1 |
| 20 | 46 | 51.1 | 954 | 2 | O9GQI5 |
| 21 | 46 | 51.1 | 969 | 2 | O9U022 |
| 22 | 45.5 | 50.6 | 381 | 1 | TH1I_METJA |
| 23 | 45 | 50.0 | 332 | 2 | O7MTQ1 |
| 24 | 45 | 50.0 | 308 | 2 | O8R2C7 |
| 25 | 45 | 50.0 | 402 | 2 | O81L43 |
| 26 | 45 | 50.0 | 834 | 2 | O7RR10 |
| 27 | 45 | 50.0 | 1634 | 1 | DPOL_METJA |
| 28 | 44 | 48.9 | 78 | 2 | O82YK7 |
| 29 | 44 | 48.9 | 93 | 2 | O64D16 |
| 30 | 44 | 48.9 | 124 | 2 | O649W3 |
| 31 | 44 | 48.9 | 125 | 2 | O64EAS |

ALIGNMENTS

| | | | | | | |
|----|----|------|------|---|------------|---------------------|
| 32 | 44 | 48.9 | 219 | 2 | O6FB91 | O6FB91 actinobact |
| 33 | 44 | 48.9 | 291 | 2 | O738Z6 | O738Z6 bacillus ce |
| 34 | 44 | 48.9 | 301 | 2 | O6H2B4 | O6H2B4 bacillus ce |
| 35 | 44 | 48.9 | 301 | 2 | O63BX5 | O63BX5 bacillus ce |
| 36 | 44 | 48.9 | 301 | 2 | O81E24 | O81E24 bacillus ce |
| 37 | 44 | 48.9 | 301 | 2 | O6H2B6 | O6H2B6 bacillus th |
| 38 | 44 | 48.9 | 303 | 2 | O81R41 | O81R41 bacillus an |
| 39 | 44 | 48.9 | 343 | 2 | O76CZ2 | O76CZ2 pyrococcus |
| 40 | 44 | 48.9 | 756 | 2 | O93XR9 | O93XR9 bruniolera g |
| 41 | 44 | 48.9 | 807 | 1 | H1S8_PHOHL | O93XR9 photorhabd |
| 42 | 44 | 48.9 | 840 | 2 | O9DHN4 | O9DHN4 yaba-like d |
| 43 | 44 | 48.9 | 1043 | 2 | O81B28 | O81B28 plasmodium |
| 44 | 44 | 48.9 | 1137 | 2 | O6LF77 | O6LF77 plasmodium |
| 45 | 44 | 48.9 | 1401 | 1 | DPQ3_THRTN | O81A32 thermoaer |

RESULT 1
ID SCS1_SHEEP STANDARD; PRT; 160 AA.
AC P49928;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Cathelin-related peptide SCS precursor 1 (Antibacterial peptide SMAP-29).
DE 29) (Myeloid antibacterial peptide SMAP-29).
DE Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Ovis.
NCBI_Taxid=9940;
RN [1]
RX MEDLINE=86140581; PubMed=8549789; DOI=10.1016/0014-5793(95)01390-3;
RT "Molecular analysis of the sheep cathelin family reveals a novel
antimicrobial peptide."
RT FEBS Lett. 377:519-522(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Huttner K.M., Mahoney M.M.;
Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Thermostable, broad spectrum, bactericidal agent.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the cathelicidin family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.ebi.ac.uk/announcements>
or send an email to license@ebi.ac.uk).
CC EMBL; X29757; CA63412.1; -
CC EMBL; U60600; AAB49715.1; -
CC PDB; 1PRY; NMR; A=132-160.
DR InterPro; IPR001894; Cathelicidin.
DR Pfam; PF00666; Cathelicidins; 1.
DR PROSITE; PS001838; Cathelicidins; 1.
DR PROSITE; PS00946; CATHELICIDINS_1; 1.
DR PROSITE; PS00947; CATHELICIDINS_2; 1.
KW 3D-structure; Antibiotic; Pyrolydine carboxylic acid; Signal.
FT SIGNAL 1 29
FT PROPEP 30 131
FT PEPTIDE 132 160
FT MOD_RSS 30 30
FT DLSUFLID 86 97
By similarity.
By similarity.
Cathelin-related peptide SCS.
Pyrolydine carboxylic acid (By
similarity).
By similarity.

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OM protein - protein search, using sw model

Run on: May 2, 2005, 13:03:56 ; Search time 48.9721 Seconds
(without alignments)
122.435 Million cell updates/sec

Title: US-09-642-744d-8

Perfect score: 90

Sequence: 1 KMLRRIIRKIIHIKKYG 18

Scoring table: BLASTSUM62
Gapop 10.0, Gapext 0.5

Searched: 1426032 seqs, 333106140 residues

Total number of hits satisfying chosen parameters: 1426032

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
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7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
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12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
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20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 2 | 90 | 100.0 | 18 | 9 | US-09-840-009-9 |
| 3 | 90 | 100.0 | 18 | 9 | US-09-840-009-16 |
| 4 | 90 | 100.0 | 18 | 9 | US-09-840-009-23 |
| 5 | 90 | 100.0 | 18 | 9 | US-09-840-009-30 |
| 6 | 90 | 100.0 | 18 | 14 | US-10-060-102-9 |
| 7 | 90 | 100.0 | 18 | 14 | US-10-060-102-12 |
| 8 | 90 | 100.0 | 18 | 15 | US-10-721-839-9 |
| 9 | 90 | 100.0 | 18 | 15 | US-10-721-839-12 |
| 10 | 90 | 100.0 | 29 | 14 | US-10-060-102-8 |
| 11 | 90 | 100.0 | 29 | 15 | US-10-721-839-8 |
| 12 | 88 | 97.8 | 18 | 14 | US-10-060-102-10 |
| 13 | 88 | 97.8 | 18 | 14 | US-10-060-102-11 |

| | | | | | | |
|----|----|------|----|----|------------------|-------------------|
| 14 | 88 | 97.8 | 18 | 15 | US-10-721-839-10 | Sequence 10, Appl |
| 15 | 88 | 97.8 | 18 | 15 | US-10-721-839-11 | Sequence 11, Appl |
| 16 | 85 | 94.4 | 18 | 9 | US-09-840-009-4 | Sequence 4, Appl |
| 17 | 85 | 94.4 | 18 | 9 | US-09-840-009-8 | Sequence 8, Appl |
| 18 | 85 | 94.4 | 18 | 9 | US-09-840-009-11 | Sequence 11, Appl |
| 19 | 85 | 94.4 | 18 | 9 | US-09-840-009-15 | Sequence 15, Appl |
| 20 | 85 | 94.4 | 18 | 9 | US-09-840-009-18 | Sequence 18, Appl |
| 21 | 85 | 94.4 | 18 | 9 | US-09-840-009-22 | Sequence 22, Appl |
| 22 | 85 | 94.4 | 18 | 9 | US-09-840-009-25 | Sequence 25, Appl |
| 23 | 85 | 94.4 | 18 | 9 | US-09-840-009-29 | Sequence 29, Appl |
| 24 | 85 | 94.4 | 18 | 14 | US-10-060-102-25 | Sequence 25, Appl |
| 25 | 85 | 94.4 | 18 | 15 | US-10-721-839-25 | Sequence 25, Appl |
| 26 | 84 | 93.3 | 18 | 9 | US-09-840-009-5 | Sequence 5, Appl |
| 27 | 84 | 93.3 | 18 | 9 | US-09-840-009-12 | Sequence 12, Appl |
| 28 | 84 | 93.3 | 18 | 9 | US-09-840-009-19 | Sequence 19, Appl |
| 29 | 84 | 93.3 | 18 | 9 | US-09-840-009-26 | Sequence 26, Appl |
| 30 | 83 | 92.2 | 18 | 9 | US-09-840-009-6 | Sequence 6, Appl |
| 31 | 83 | 92.2 | 18 | 9 | US-09-840-009-7 | Sequence 7, Appl |
| 32 | 83 | 92.2 | 18 | 9 | US-09-840-009-13 | Sequence 13, Appl |
| 33 | 83 | 92.2 | 18 | 9 | US-09-840-009-14 | Sequence 14, Appl |
| 34 | 83 | 92.2 | 18 | 9 | US-09-840-009-20 | Sequence 20, Appl |
| 35 | 83 | 92.2 | 18 | 9 | US-09-840-009-21 | Sequence 21, Appl |
| 36 | 83 | 92.2 | 18 | 9 | US-09-840-009-27 | Sequence 27, Appl |
| 37 | 83 | 92.2 | 18 | 9 | US-09-840-009-28 | Sequence 28, Appl |
| 38 | 82 | 91.1 | 18 | 9 | US-09-840-009-3 | Sequence 3, Appl |
| 39 | 82 | 91.1 | 18 | 9 | US-09-840-009-10 | Sequence 10, Appl |
| 40 | 82 | 91.1 | 18 | 9 | US-09-840-009-17 | Sequence 17, Appl |
| 41 | 82 | 91.1 | 18 | 9 | US-09-840-009-24 | Sequence 24, Appl |
| 42 | 82 | 91.1 | 18 | 9 | US-09-840-009-31 | Sequence 31, Appl |
| 43 | 82 | 91.1 | 18 | 14 | US-10-060-102-26 | Sequence 26, Appl |
| 44 | 82 | 91.1 | 18 | 14 | US-10-077-624-17 | Sequence 17, Appl |
| 45 | 82 | 91.1 | 18 | 15 | US-10-721-839-26 | Sequence 26, Appl |

ALIGNMENTS

RESULT 1
US-09-840-009-2
; Sequence 2, Application US/09840009
; Patent No. US20020082195A1
; GENERAL INFORMATION:
; APPLICANT: Lehrer, Robert I.
; APPLICANT: Waring, Alan J.
; APPLICANT: Tack, Brian F.
; FILE REFERENCE: 06510-195W0
; CURRENT APPLICATION NUMBER: US/09/840,009
; PRIOR FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 09/606,858
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic antimicrobial peptide
US-09-840-009-2

Query Match 100.0%; Score 90; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

QY 1 KMLRRIIRKIIHIKKYG 18
DB 1 KMLRRIIRKIIHIKKYG 18

RESULT 2
US-09-840-009-9
; Sequence 9, Application US/09840009

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OM protein - protein search, using sw model

Run on: May 2, 2005, 12:18:40 ; Search time 17.095 Seconds

(without alignments)
78.601 Million cell updates/sec

Title: US-09-642-744d-8

Sequence: 1 KNLRRIRKIHIIKKYG 18

Scoring table:

BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74643064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: /cgnt2_6/prodata/1/iaa/5B_COMB.pep.*
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4: /cgnt2_6/prodata/1/iaa/6B_COMB.pep.*
5: /cgnt2_6/prodata/1/iaa/PCITUS_COMB.pep.*
6: /cgnt2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|------------------|
| 1 | 90 | 100.0 | 18 | 4 | US-09-840-009-2 |
| 2 | 90 | 100.0 | 18 | 4 | US-09-840-009-9 |
| 3 | 90 | 100.0 | 18 | 4 | US-09-840-009-16 |
| 4 | 90 | 100.0 | 18 | 4 | US-09-840-009-23 |
| 5 | 90 | 100.0 | 18 | 4 | US-09-840-009-30 |
| 6 | 85 | 94.4 | 18 | 4 | US-09-840-009-4 |
| 7 | 85 | 94.4 | 18 | 4 | US-09-840-009-8 |
| 8 | 85 | 94.4 | 18 | 4 | US-09-840-009-11 |
| 9 | 85 | 94.4 | 18 | 4 | US-09-840-009-15 |
| 10 | 85 | 94.4 | 18 | 4 | US-09-840-009-18 |
| 11 | 85 | 94.4 | 18 | 4 | US-09-840-009-22 |
| 12 | 85 | 94.4 | 18 | 4 | US-09-840-009-25 |
| 13 | 85 | 94.4 | 18 | 4 | US-09-840-009-29 |
| 14 | 84 | 93.3 | 18 | 4 | US-09-840-009-5 |
| 15 | 84 | 93.3 | 18 | 4 | US-09-840-009-12 |
| 16 | 84 | 93.3 | 18 | 4 | US-09-840-009-19 |
| 17 | 84 | 93.3 | 18 | 4 | US-09-840-009-26 |
| 18 | 83 | 92.2 | 18 | 4 | US-09-840-009-7 |
| 19 | 83 | 92.2 | 18 | 4 | US-09-840-009-13 |
| 20 | 83 | 92.2 | 18 | 4 | US-09-840-009-20 |
| 21 | 83 | 92.2 | 18 | 4 | US-09-840-009-21 |
| 22 | 83 | 92.2 | 18 | 4 | US-09-840-009-27 |
| 23 | 83 | 92.2 | 18 | 4 | US-09-840-009-28 |
| 24 | 83 | 92.2 | 18 | 4 | US-09-840-009-3 |
| 25 | 83 | 92.2 | 18 | 4 | US-09-840-009-10 |
| 26 | 82 | 91.1 | 18 | 4 | US-09-840-009-17 |
| 27 | 82 | 91.1 | 18 | 4 | US-09-840-009-24 |

| | | | | | | |
|----|------|------|-----|---|----------------------|--------------------|
| 28 | 82 | 91.1 | 18 | 4 | US-09-840-009-17 | Sequence 17, Appl |
| 29 | 82 | 91.1 | 18 | 4 | US-09-840-009-24 | Sequence 24, Appl |
| 30 | 82 | 91.1 | 18 | 4 | US-09-840-009-31 | Sequence 31, Appl |
| 31 | 76 | 84.4 | 18 | 4 | US-09-840-009-34 | Sequence 34, Appl |
| 32 | 76 | 84.4 | 18 | 4 | US-09-840-009-35 | Sequence 35, Appl |
| 33 | 74 | 82.2 | 18 | 4 | US-09-840-009-33 | Sequence 33, Appl |
| 34 | 74 | 82.2 | 18 | 4 | US-09-840-009-33 | Sequence 33, Appl |
| 35 | 70 | 77.8 | 18 | 4 | US-09-840-009-1 | Sequence 1, Appl |
| 36 | 65 | 72.2 | 18 | 4 | US-09-840-009-36 | Sequence 36, Appl |
| 37 | 65 | 72.2 | 18 | 4 | US-09-840-009-37 | Sequence 37, Appl |
| 38 | 57 | 63.3 | 160 | 4 | US-09-917-340-36 | Sequence 36, Appl |
| 39 | 50 | 55.6 | 169 | 4 | US-09-270-767-35406 | Sequence 35406, A |
| 40 | 50 | 55.6 | 169 | 4 | US-09-270-767-350623 | Sequence 350623, A |
| 41 | 50 | 55.6 | 205 | 3 | US-09-134-001C-4766 | Sequence 4766, Ap |
| 42 | 43.5 | 48.3 | 167 | 4 | US-09-110-279-1502 | Sequence 1502, Ap |
| 43 | 43.5 | 48.3 | 320 | 3 | US-09-134-001C-3823 | Sequence 3823, Ap |
| 44 | 43 | 47.8 | 823 | 4 | US-09-949-016-8339 | Sequence 8339, Ap |
| 45 | 42 | 46.7 | 24 | 4 | US-09-785-059B-5 | Sequence 5, Appl |

ALIGNMENTS

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RESULT 1
US-09-840-009-2
; Sequence 2, Application US/09840009
; Patent No. 6492328
; GENERAL INFORMATION:
; APPLICANT: Lehrer, Robert I.
; APPLICANT: Waring, Alan J.
; APPLICANT: Tack, Brian F.
; TITLE OF INVENTION: NOVISPRINS: ANTIMICROBIAL PEPTIDES
; FILE REFERENCE: 06510-195W0
; CURRENT APPLICATION NUMBER: US/09/840,009
; PRIOR FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 09/606,858
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic antimicrobial peptide
US-09-840-009-2
Query Match          100.0%; Score 90; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KNLRRIRKIHIIKKYG 18
Db       1 KNLRRIRKIHIIKKYG 18

RESULT 2
US-09-840-009-9
; Sequence 9, Application US/09840009
; Patent No. 6492328
; GENERAL INFORMATION:
; APPLICANT: Lehrer, Robert I.
; APPLICANT: Waring, Alan J.
; APPLICANT: Tack, Brian F.
; TITLE OF INVENTION: NOVISPRINS: ANTIMICROBIAL PEPTIDES
; FILE REFERENCE: 06510-195W0
; CURRENT APPLICATION NUMBER: US/09/840,009
; PRIOR FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: US 09/606,858
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 2, 2005, 12:17:55 ; Search time 63.1006 Seconds

(without alignments)
110.327 Million cell updates/sec

Title: US-09-642-744d-8

Perfect score: 90

Sequence: 1 KNLRRIRIKIHIKKYG 18

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 10%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|------------|---------------------|
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| 2 | 90 | 100.0 | 18 | 4 AAB70648 | Aab70648 Ovine SMA |
| 3 | 90 | 100.0 | 18 | 5 AAE20882 | Aae20882 D11-novi |
| 4 | 90 | 100.0 | 18 | 5 AAE20875 | Aae20875 D11-novi |
| 5 | 90 | 100.0 | 18 | 5 AAE20854 | Aae20854 Ovipirrin |
| 6 | 90 | 100.0 | 18 | 5 AAE20861 | Aae20861 D16-novis |
| 7 | 90 | 100.0 | 18 | 5 AAE20868 | Aae20868 D17-novis |
| 8 | 90 | 100.0 | 18 | 5 ABP53276 | Abp53276 Synthetic |
| 9 | 90 | 100.0 | 18 | 5 ABP53279 | Abp53279 Synthetic |
| 10 | 90 | 100.0 | 29 | 4 AAB70675 | Aab70675 Ovine SMA |
| 11 | 90 | 100.0 | 29 | 5 ABP53275 | Abp53275 Synthetic |
| 12 | 88 | 97.8 | 18 | 4 AAB70654 | Aab70654 Ovine SMA |
| 13 | 88 | 97.8 | 18 | 5 ABP53278 | Abp53278 Synthetic |
| 14 | 88 | 97.8 | 18 | 5 ABP53277 | Abp53277 Synthetic |
| 15 | 88 | 97.8 | 20 | 4 AAB70653 | Aab70653 Ovine SMA |
| 16 | 85 | 94.4 | 18 | 5 AAE20870 | Aae20870 T10-novis |
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| 19 | 85 | 94.4 | 18 | 5 AAE20867 | Aae20867 D17-novis |
| 20 | 85 | 94.4 | 18 | 5 AAE20874 | Aae20874 D10-novi |
| 21 | 85 | 94.4 | 18 | 5 AAE20863 | Aae20863 T7-novisp |
| 22 | 85 | 94.4 | 18 | 5 AAE20877 | Aae20877 T11-novisp |
| 23 | 85 | 94.4 | 18 | 5 AAE20856 | Aae20856 T6-novisp |
| 24 | 85 | 94.4 | 18 | 5 ABP53292 | Abp53292 Synthetic |
| 25 | 84 | 93.3 | 18 | 5 AAE20864 | Aae20864 S7-novisp |

ALIGNMENTS

| | | | | | |
|----|----|------|----|------------|--------------------|
| 26 | 84 | 93.3 | 18 | 5 AAE20871 | Aae20871 S10-novis |
| 27 | 84 | 93.3 | 18 | 5 AAE20878 | Aae20878 S11-novis |
| 28 | 84 | 93.3 | 18 | 5 AAE20857 | Aae20857 S6-novisp |
| 29 | 83 | 92.2 | 18 | 5 AAE20872 | Aae20872 E10-novis |
| 30 | 83 | 92.2 | 18 | 5 AAE20873 | Aae20873 D10-novis |
| 31 | 83 | 92.2 | 18 | 5 AAE20858 | Aae20858 E6-novisp |
| 32 | 83 | 92.2 | 18 | 5 AAE20866 | Aae20866 D7-novisp |
| 33 | 83 | 92.2 | 18 | 5 AAE20879 | Aae20879 E11-novis |
| 34 | 83 | 92.2 | 18 | 5 AAE20865 | Aae20865 E7-novisp |
| 35 | 83 | 92.2 | 18 | 5 AAE20880 | Aae20880 D11-novis |
| 36 | 83 | 92.2 | 18 | 5 AAE20859 | Aae20859 D6-novisp |
| 37 | 82 | 91.1 | 18 | 5 AAE20862 | Aae20862 G7-novisp |
| 38 | 82 | 91.1 | 18 | 5 AAE20876 | Aae20876 G11-novis |
| 39 | 82 | 91.1 | 18 | 5 AAE20883 | Aae20883 G10-novis |
| 40 | 82 | 91.1 | 18 | 5 AAE20869 | Aae20869 G10-novis |
| 41 | 82 | 91.1 | 18 | 5 AAE20855 | Aae20855 G6-novisp |
| 42 | 82 | 91.1 | 18 | 5 ABP53293 | Abp53293 Synthetic |
| 43 | 82 | 91.1 | 18 | 6 ABP72293 | Abp72293 Antimicro |
| 44 | 82 | 91.1 | 18 | 8 ADQ15520 | Adq15520 Antimicro |
| 45 | 82 | 91.1 | 36 | 8 ADQ15575 | Adq15575 Novispri |

RESULT 1
AAB70655
ID AAB70655 standard; peptide; 18 AA.
AC AAB70655;
DT 15-MAY-2001 (first entry)
XX
DE Ovine SNAP 29 cathelicidin derived antimicrobial peptide SEQ ID NO:8.
XX
KW Ovine; SNAP29; lupine; RCAP 18; cathelicidin; antimicrobial;
KW bactericidal; antibiotic; antiviral; microbial growth inhibitor;
KW proliferation inhibitor; gene therapy; Pseudomonas aeruginosa;
KW Burkholderia cepacia; Alcaligenes; Xanthomonas.
XX
OS Ovis aries.
XX
PN WO200112668-A1.
XX
PD 22-FEB-2001.
XX
PF 18-AUG-2000; 2000WO-US022781.
XX
PR 18-AUG-1999; 99US-0149886P.
XX
PA (TOWA) UNIV IOWA RES FOUND.
PA (REGC) UNIV CALIFORNIA.
XX
PI Track BE, Mccray P, Welsh M, Travis SM, Lehrer R;
XX WPI; 2001-234911/24.
XX
DR New antimicrobial peptides useful as antibiotics for inhibiting growth
XX PT and proliferation of microbes, and for treating microbial infections.
XX PS Claim 1, Page 103; 137pp; English.
XX
CC AAB70648 to AAB70675 represent antimicrobial peptides (I), of which
CC AAB70648 to AAB70664, AAB70674 and AAB70675 are derived from the ovine
CC SNAP 29 cathelicidin family peptide, and AAB70665 to AAB70673 are derived
CC from the lupine RCAP 18 cathelicidin family peptide. (I) have antibiotic,
CC antimicrobial and antiviral activities, and can be used as microbial
CC growth and proliferation inhibitors and in gene therapy. (II) are useful
CC for inhibiting microbial growth in an environment capable of sustaining
CC such growth, for inhibiting microbial growth or strain in a host, and
CC inhibiting the growth of drug-resistant microbial strains such as
CC Pseudomonas aeruginosa, Burkholderia cepacia, Alcaligenes and Xanthomonas
XX